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(54) Title: AN IMPROVED CLEANING COMPOSITION			
(57) Abstract <p>Novel alpha-amylase mutants derived from the DNA sequences of naturally occurring or recombinant alpha-amylases are disclosed. The mutant alpha-amylases, in general, are obtained by <i>in vitro</i> modifications of a precursor DNA sequence encoding the naturally occurring or recombinant alpha-amylase to generate the substitution (replacement) or deletion of one or more oxidizable amino acid residues in the amino acid sequence of a precursor alpha-amylase. Such mutant alpha-amylases have altered oxidative stability and/or altered pH performance profiles and/or altered thermal stability as compared to the precursor. Also disclosed are detergent and starch liquefaction compositions comprising the mutant amylases, as well as methods of using the mutant amylases. More particularly preferred are mutant alpha-amylases from <i>Bacillus licheniformis</i> modified at MET197 or MET15 or at TRP138 residues or at equivalent residues of other alpha-amylases from other microbial sources (<i>Bacillus, Aspergillus</i>).</p>			

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AN IMPROVED CLEANING COMPOSITION

Field of the Invention

The present invention relates to novel alpha-amylase mutants having an amino acid sequence not found in nature, such mutants having an amino acid sequence wherein one or more amino acid residue(s) of a precursor alpha-amylase, specifically any oxidizable amino acid, have been substituted with a different amino acid. The mutant enzymes of the present invention exhibit altered stability/activity profiles including but not limited to altered oxidative stability, altered pH performance profile, altered specific activity and/or altered thermostability.

Background of the Invention

Alpha-amylases (alpha-1,4-glucan-4-glucanohydrolase, EC3.2.1.1) hydrolyze internal alpha-1,4-glucosidic linkages in starch largely at random, to produce smaller molecular weight malto-dextrins. Alpha-amylases are of considerable commercial value, being used in the initial stages (liquefaction) of starch processing; in alcohol production; as cleaning agents in detergent matrices; and in the textile industry for starch desizing. Alpha-amylases are produced by a wide variety of microorganisms including *Bacillus* and *Aspergillus*, with most commercial amylases being produced from bacterial sources such as *B. licheniformis*, *B. amyloliquefaciens*, *B. subtilis*, or *B. stearothermophilus*. In recent years the preferred enzymes in commercial use have been those from *B. licheniformis* because of their heat stability and performance, at least at neutral and mildly alkaline pH's.

Previously there have been studies using recombinant DNA techniques to explore which residues are important for the catalytic activity of amylases and/or to explore the effect of modifying certain amino acids within the active site of various amylases (Vihinen, M. et al. (1990) *J. Biochem.* 107:267-272; Holm, L. et al. (1990) *Protein Engine* 3:181-191; Takase, K. et al. (1992) *Biochimica et Biophysica Acta*, 1120:281-288; Matsui, I. et al. (1992) *FEBS Letters*

Vol. 310, No. 3, pp. 216-218); which residues are important for thermal stability (Suzuki, Y. et al. (1989) J. Biol. Chem. 264:18933-18938); and one group has used such methods to introduce mutations at various histidine residues in a *B. licheniformis* amylase, the rationale for making substitutions at histidine residues was that *B. licheniformis* amylase (known to be thermostable) when compared to other similar *Bacillus* amylases, has an excess of histidines and, therefore, it was suggested that replacing a histidine could affect the thermostability of the enzyme (Declerck, N. et al. (1990) J. Biol. Chem. 265:15481-15488; FR 2 665 178-A1; Joyet, P. et al. (1992) Bio/Technology 10:1579-1583).

It has been found that alpha-amylase is inactivated by hydrogen peroxide and other oxidants at pH's between 4 and 10.5 as described in the examples herein. Commercially, alpha-amylase enzymes can be used under dramatically different conditions such as both high and low pH conditions, depending on the commercial application. For example, alpha-amylases may be used in the liquefaction of starch, a process preferably performed at a low pH (pH <5.5). On the other hand, amylases may be used in commercial dish care or laundry detergents, which often contain oxidants such as bleach or peracids, and which are used in much more alkaline conditions.

In order to alter the stability or activity profile of amylase enzymes under varying conditions, it has been found that selective replacement, substitution or deletion of oxidizable amino acids, such as a methionine, tryptophan, tyrosine, histidine or cysteine, results in an altered profile of the variant enzyme as compared to its precursor. Because currently commercially available amylases are not acceptable (stable) under various conditions, there is a need for an amylase having an altered stability and/or activity profile. This altered stability (oxidative, thermal or pH performance profile) can be achieved while maintaining adequate enzymatic activity, as compared to the wild-type or precursor enzyme. The characteristic affected by introducing such mutations may be a change in oxidative stability while maintaining thermal stability or vice versa. Additionally, the substitution of different amino acids for an oxidizable amino acid in the alpha-amylase precursor sequence or the deletion of one or more oxidizable amino acid(s) may result in altered enzymatic activity at a pH other than that which is considered optimal for the precursor alpha-

amylase. In other words, the mutant enzymes of the present invention may also have altered pH performance profiles, which may be due to the enhanced oxidative stability of the enzyme.

Summary of the Invention

The present invention relates to novel alpha-amylase mutants that are the expression product of a mutated DNA sequence encoding an alpha-amylase, the mutated DNA sequence being derived from a precursor alpha-amylase by the deletion or substitution (replacement) of one or more oxidizable amino acid. In one preferred embodiment of the present invention the mutant results from substituting a different amino acid for one or more methionine residue(s) in the precursor alpha-amylase. In another embodiment of the present invention the mutants comprise a substitution of one or more tryptophan residue alone or in combination with the substitution of one or more methionine residue in the precursor alpha-amylase. Such mutant alpha-amylases, in general, are obtained by *in vitro* modification of a precursor DNA sequence encoding a naturally occurring or recombinant alpha-amylase to encode the substitution or deletion of one or more amino acid residues in a precursor amino acid sequence.

Preferably the substitution or deletion of one or more amino acid in the amino acid sequence is due to the replacement or deletion of one or more methionine, tryptophan, cysteine, histidine or tyrosine residues in such sequence, most preferably the residue which is changed is a methionine residue. The oxidizable amino acid residues may be replaced by any of the other 20 naturally occurring amino acids. If the desired effect is to alter the oxidative stability of the precursor, the amino acid residue may be substituted with a non-oxidizable amino acid (such as alanine, arginine, asparagine, aspartic acid, glutamic acid, glutamine, glycine, isoleucine, leucine, lysine, phenylalanine, proline, serine, threonine, or valine) or another oxidizable amino acid (such as cysteine, methionine, tryptophan, tyrosine or histidine, listed in order of most easily oxidizable to less readily oxidizable). Likewise, if the desired effect is to alter thermostability, any of the other 20 naturally occurring amino acids may be substituted (i.e., cysteine may be substituted for methionine).

Preferred mutants comprise the substitution of a methionine residue equivalent to any of the methionine residues found in *B. licheniformis* alpha-amylase (+8, +15, +197, +256, +304, +366 and +438). Most preferably the methionine to be replaced is a methionine at a position equivalent to position +197 or +15 in *B. licheniformis* alpha-amylase. Preferred substitute amino acids to replace the methionine at position +197 are alanine (A), isoleucine (I), threonine (T) or cysteine (C). The preferred substitute amino acids at position +15 are leucine (L), threonine (T), asparagine (N), aspartate (D), serine (S), valine (V) and isoleucine (I), although other substitute amino acids not specified above may be useful. Two specifically preferred mutants of the present invention are M197T and M15L.

Another embodiment of this invention relates to mutants comprising the substitution of a tryptophan residue equivalent to any of the tryptophan residues found in *B. licheniformis* alpha-amylase (see Fig. 2). Preferably the tryptophan to be replaced is at a position equivalent to +138 in *B. licheniformis* alpha-amylase. A mutation (substitution) at a tryptophan residue may be made alone or in combination with mutations at other oxidizable amino acid residues. Specifically, it may be advantageous to modify by substitution at least one tryptophan in combination with at least one methionine (for example, the double mutant +138/+197).

The alpha-amylase mutants of the present invention, in general, exhibit altered oxidative stability in the presence of hydrogen peroxide and other oxidants such as bleach or peracids, or, more specific, milder oxidants such as chloramine-T. Mutant enzymes having enhanced oxidative stability will be useful in extending the shelf life and bleach, perborate, percarbonate or peracid compatibility of amylases used in cleaning products. Similarly, reduced oxidative stability may be useful in industrial processes that require the rapid and efficient quenching of enzymatic activity. The mutant enzymes of the present invention may also demonstrate a broadened pH performance profile whereby mutants such as M15L show stability for low pH starch liquefaction and mutants such as M197T show stability at high pH cleaning product conditions. The mutants of the present invention may also have altered thermal stability whereby the mutant may have enhanced stability at either high or low temperatures. It is understood that any change

(increase or decrease) in the mutant's enzymatic characteristic(s), as compared to its precursor, may be beneficial depending on the desired end use of the mutant alpha-amylase.

In addition to starch processing and cleaning applications, variant amylases of the present invention may be used in any application in which known amylases are used, for example, variant amylases can be used in textile processing, food processing, etc. Specifically, it is contemplated that a variant enzyme such as M197C, which is easily inactivated by oxidation, would be useful in a process where it is desirable to completely remove amylase activity at the end of the process, for example, in frozen food processing applications.

The preferred alpha-amylase mutants of the present invention are derived from a *Bacillus* strain such as *B. licheniformis*, *B. amyloliquefaciens*, and *B. stearothermophilus*, and most preferably from *Bacillus licheniformis*.

In another aspect of the present invention there is provided a novel form of the alpha-amylase normally produced by *B. licheniformis*. This novel form, designated as the A4 form, has an additional four alanine residues at the N-terminus of the secreted amylase. (Fig. 4b.) Derivatives or mutants of the A4 form of alpha-amylase are encompassed within the present invention. By derivatives or mutants of the A4 form, it is meant that the present invention comprises the A4 form alpha-amylase containing one or more additional mutations such as, for example, mutation (substitution, replacement or deletion) of one or more oxidizable amino acid(s).

In a composition embodiment of the present invention there are provided detergent compositions, liquid, gel or granular, comprising the alpha-amylase mutants described herein. Particularly preferred are detergent compositions comprising a +197 position mutant either alone or in combination with other enzymes such as endoglycosidases, cellulases, proteases, lipases or other amylase enzymes. Additionally, it is contemplated that the compositions of the present invention may include an alpha-amylase mutant having more than one site-specific mutation.

In yet another composition embodiment of the present invention there are provided compositions useful in starch processing and

particularly starch liquefaction. The starch liquefaction compositions of the present invention preferably comprise an alpha-amylase mutant having a substitution or deletion at position M15. Additionally, it is contemplated that such compositions may comprise additional components as known to those skilled in the art, including, for example, antioxidants, calcium, ions, etc.

In a process aspect of the present invention there are provided methods for liquefying starch, and particularly granular starch slurries, from either a wet or dry milled process. Generally, in the first step of the starch degradation process, the starch slurry is gelatinized by heating at a relatively high temperature (up to about 110°C). After the starch slurry is gelatinized it is liquefied and dextrinized using an alpha-amylase. The conditions for such liquefaction are described in commonly assigned US patent applications 07/785,624 and 07/785,623 and US Patent 5,180,669, the disclosure of which are incorporated herein by reference. The present method for liquefying starch comprises adding to a starch slurry an effective amount of an alpha-amylase of the present invention, alone or in combination with additional excipients such as an antioxidant, and reacting the slurry for an appropriate time and temperature to liquefy the starch.

A further aspect of the present invention comprises the DNA encoding the mutant alpha-amylases of the present invention (including A4 form and mutants thereof) and expression vectors encoding the DNA as well as host cells transformed with such expression vectors.

Brief Description of the Drawings

Fig. 1 shows the DNA sequence of the gene for alpha-amylase from *B. licheniformis* (NCIB8061), Seq ID No 31, and deduced translation product as described in Gray, G. et al. (1986) J. Bacter. 166:635-643.

Fig. 2 shows the amino acid sequence of the mature alpha-amylase enzyme from *B. licheniformis* (NCIB8061), Seq ID No 32.

Fig. 3 shows an alignment of primary structures of *Bacillus* alpha-amylases. The *B. licheniformis* amylase (Am-Lich), Seq ID No 33, is described by Gray, G. et al. (1986) J. Bact. 166:635-643; the *B. amyloliquefaciens* amylase (Am-Amylo), Seq ID No 34, is described by

Takkinen, K. et al. (1983) J. Biol. Chem. 258:1007-1013; and the *B. stearothermophilus* (Am-St aro), Seq ID No 35, is described by Ihara, H. et al. (1985) J. Biochem. 98:95-103.

Fig. 4a shows the amino acid sequence of the mature alpha-amylase variant M197T, Seq ID No 36.

Fig. 4b shows the amino acid sequence of the A4 form of alpha-amylase from *B. licheniformis* NCIB8061, Seq ID No 37. Numbering is from the N-terminus, starting with the four additional alanines.

Fig. 5 shows plasmid pA4BL wherein BLAA refers to *B. licheniformis* alpha-amylase gene, PstI to SstI; Amp^r refers to the ampicillin-resistant gene from pBR322; and CAT refers to the Chloramphenicol-resistant gene from pC194.

Fig. 6 shows the signal sequence-mature protein junctions for *B. licheniformis* (Seq ID No 38), *B. subtilis* (Seq ID No 39), *B. licheniformis* in pA4BL (Seq ID No 40) and *B. licheniformis* in pBLapr (Seq ID No 41).

Fig. 7a shows inactivation of certain alpha-amylases (Spezyme® AA20 and M197L (A4 form) with 0.88M H₂O₂ at pH 5.0, 25°C.

Fig. 7b shows inactivation of certain alpha-amylases (Spezyme® AA20, M197T) with 0.88M H₂O₂ at pH 10.0, 25°C.

Fig. 7c shows inactivation of certain alpha-amylases (Spezyme® AA20, M15L) with 0.88M H₂O₂ at pH 5.0, 25°C.

Fig. 8 shows a schematic for the production of M197X cassette mutants.

Fig. 9 shows expression of M197X variants.

Fig. 10 shows thermal stability of M197X variants at pH 5.0, 5mM CaCl₂ at 95°C for 5 mins.

Figs. 11a and 11b show inactivation of certain amylases in automatic dish care detergents. Fig. 11a shows the stability of certain amylases in Cascade™ (a commercially available dish car product) at

65°C in the presence or absence of starch. Fig. 11b shows the stability of certain amylases in Sunlight™ (a commercially available dish care product) at 65°C in the presence or absence of starch.

Fig. 12 shows a schematic for the production of M15X cassette mutants.

Fig. 13 shows expression of M15X variants.

Fig. 14 shows specific activity of M15X variants on soluble starch.

Fig. 15 shows heat stability of M15X variants at 90°C, pH 5.0, 5mM CaCl₂, 5 mins.

Fig. 16 shows specific activity on starch and soluble substrate, and performance in jet liquefaction at pH 5.5, of M15 variants as a function of percent activity of *B. licheniformis* wild-type.

Fig. 17 shows the inactivation of *B. licheniformis* alpha-amylase (AA20 at 0.65 mg/ml) with chloramine-T at pH 8.0 as compared to variants M197A (1.7 mg/ml) and M197L (1.7 mg/ml).

Fig. 18 shows the inactivation of *B. licheniformis* alpha-amylase (AA20 at 0.22 mg/ml) with chloramine-T at pH 4.0 as compared to variants M197A (4.3 mg/ml) and M197L (0.53 mg/ml).

Fig. 19 shows the reaction of *B. licheniformis* alpha-amylase (AA20 at 0.75 mg/ml) with chloramine-T at pH 5.0 as compared to double variants M197T/W138F (0.64 mg/ml) and M197T/W138Y (0.60 mg/ml).

Fig. 20 shows the stability testing results of various alpha-amylase multiple mutants incorporated in automatic dish detergent (ADD) formulations at temperatures from room temperature increased to 65°C.

Fig. 21 shows the stability of certain amylase mutants (compared to wild-type) in an automatic dish detergent at room temperature over 0-30 days, as determined by percent activity remaining over time.

Fig. 22 shows the stability of certain amylase mutants (compared to wild-type) in an automatic dish detergent at 38°C (100°F) with 80% relative humidity over 0-30 days.

Detailed Description of the Invention

It is believed that amylases used in starch liquefaction may be subject to some form of inactivation due to some activity present in the starch slurry (see commonly owned US applications 07/785,624 and 07/785,623 and US Patent 5,180,669, issued January 19, 1993, incorporated herein by reference). Furthermore, use of an amylase in the presence of oxidants, such as in bleach- or peracid-containing detergents, may result in partial or complete inactivation of the amylase. Therefore, the present invention focuses on altering the oxidative sensitivity of amylases. The mutant enzymes of the present invention may also have an altered pH profile and/or altered thermal stability which may be due to the enhanced oxidative stability of the enzyme at low or high pH's.

Alpha-amylase as used herein includes naturally occurring amylases as well as recombinant amylases. Preferred amylases in the present invention are alpha-amylases derived from *B. licheniformis* or *B. stearothermophilus*, including the A4 form of alpha-amylase derived from *B. licheniformis* as described herein, as well as fungal alpha-amylases such as those derived from *Aspergillus* (i.e., *A. oryzae* and *A. niger*).

Recombinant alpha-amylases refers to an alpha-amylase in which the DNA sequence encoding the naturally occurring alpha-amylase is modified to produce a mutant DNA sequence which encodes the substitution, insertion or deletion of one or more amino acids in the alpha-amylase sequence. Suitable modification methods are disclosed herein, and also in commonly owned US Patents 4,760,025 and 5,185,258, the disclosure of which are incorporated herein by reference.

Homologies have been found between almost all endo-amylases sequenced to date, ranging from plants, mammals, and bacteria (Nakajima, R.T. et al. (1986) Appl. Microbiol. Biotechnol. 23:355-360; Rogers, J.C. (1985) Biochem. Biophys. Res. Commun. 128:470-476). There are four areas of particularly high homology in certain *Bacillus amylas* s, as shown in Fig. 3, wherein the underlined

sections designated the areas of high homology. Further, sequence alignments have been used to map the relationship between *Bacillus* endo-amylases (Feng, D.F. and Doolittle, R.F. (1987) *J. Molec. Evol.* 35:351-360). The relative sequence homology between *B. stearothermophilus* and *B. licheniformis* amylase is about 66%, as determined by Holm, L. et al. (1990) *Protein Engineering* 3 (3) pp. 181-191. The sequence homology between *B. licheniformis* and *B. amyloliquefaciens* amylases is about 81%, as per Holm, L. et al., *supra*. While sequence homology is important, it is generally recognized that structural homology is also important in comparing amylases or other enzymes. For example, structural homology between fungal amylases and bacterial (*Bacillus*) amylase have been suggested and, therefore, fungal amylases are encompassed within the present invention.

An alpha-amylase mutant has an amino acid sequence which is derived from the amino acid sequence of a precursor alpha-amylase. The precursor alpha-amylases include naturally occurring alpha-amylases and recombinant alpha-amylases (as defined). The amino acid sequence of the alpha-amylase mutant is derived from the precursor alpha-amylase amino acid sequence by the substitution, deletion or insertion of one or more amino acids of the precursor amino acid sequence. Such modification is of the precursor DNA sequence which encodes the amino acid sequence of the precursor alpha-amylase rather than manipulation of the precursor alpha-amylase enzyme *per se*. Suitable methods for such manipulation of the precursor DNA sequence include methods disclosed herein and in commonly owned US patent 4,760,025 and 5,185,258.

Specific residues corresponding to positions M197, M15 and W138 of *Bacillus licheniformis* alpha-amylase are identified herein for substitution or deletion, as are all methionine, histidine, tryptophan, cysteine and tyrosine positions. The amino acid position number (i.e., +197) refers to the number assigned to the mature *Bacillus licheniformis* alpha-amylase sequence presented in Fig. 2. The invention, however, is not limited to the mutation of this particular mature alpha-amylase (*B. licheniformis*) but extends to precursor alpha-amylases containing amino acid residues at positions which are equivalent to the particular identified residue in *B. licheniformis* alpha-amylase. A residue (amino acid) of a precursor alpha-amylase is equivalent to a residue of *B.*

licheniformis alpha-amylase if it is either homologous (i.e., corresponding in position in either primary or tertiary structure) or analogous to a specific residue or portion of that residue in *B. licheniformis* alpha-amylase (i.e., having the same or similar functional capacity to combine, react, or interact chemically or structurally).

In order to establish homology to primary structure, the amino acid sequence of a precursor alpha-amylase is directly compared to the *B. licheniformis* alpha-amylase primary sequence and particularly to a set of residues known to be invariant to all alpha-amylases for which sequence is known, as seen in Fig. 3. It is possible also to determine equivalent residues by tertiary structure: crystal structures have been reported for porcine pancreatic alpha-amylase (Buisson, G. et al. (1987) EMBO J. 6:3909-3916); Taka-amylase A from *Aspergillus oryzae* (Matsuura, Y. et al. (1984) J. Biochem. (Tokyo) 95:697-702); and an acid alpha-amylase from *A. niger* (Boel, E. et al. (1990) Biochemistry 29:6244-6249), with the former two structures being similar. There are no published structures for *Bacillus* alpha-amylases, although there are predicted to be common super-secondary structures between glucanases (MacGregor, E.A. & Svensson, B. (1989) Biochem. J. 259:145-152) and a structure for the *B. stearothermophilus* enzyme has been modeled on that of Taka-amylase A (Holm, L. et al. (1990) Protein Engineering 3:181-191). The four highly conserved regions shown in Fig. 3 contain many residues thought to be part of the active-site (Matsuura, Y. et al. (1984) J. Biochem. (Tokyo) 95:697-702; Buisson, G. et al. (1987) EMBO J. 6:3909-3916; Vihinen, M. et al. (1990) J. Biochem. 107:267-272) including, in the *licheniformis* numbering, His105; Arg229; Asp231; His235; Glu261 and Asp328.

Expression vector as used herein refers to a DNA construct containing a DNA sequence which is operably linked to a suitable control sequence capable of effecting the expression of said DNA in a suitable host. Such control sequences may include a promoter to effect transcription, an optional operator sequence to control such transcription, a sequence encoding suitable mRNA ribosome-binding sites, and sequences which control termination of transcription and translation. A preferred promoter is the *B. subtilis* *aprE* promoter. The vector may be a plasmid, a phage particle, or simply a potential genomic insert. Once transformed into a suitable host, the vector

may replicate and function independently of the host genome, or may, in some instances, integrate into the genome itself. In the present specification, plasmid and vector are sometimes used interchangeably as the plasmid is the most commonly used form of vector at present. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which are, or become, known in the art.

Host strains (or cells) useful in the present invention generally are procaryotic or eucaryotic hosts and include any transformable microorganism in which the expression of alpha-amylase can be achieved. Specifically, host strains of the same species or genus from which the alpha-amylase is derived are suitable, such as a *Bacillus* strain. Preferably an alpha-amylase negative *Bacillus* strain (genes deleted) and/or an alpha-amylase and protease deleted *Bacillus* strain such as *Bacillus subtilis* strain BG2473 ($\Delta amyE, \Delta apr, \Delta npr$) is used. Host cells are transformed or transfected with vectors constructed using recombinant DNA techniques. Such transformed host cells are capable of either replicating vectors encoding the alpha-amylase and its variants (mutants) or expressing the desired alpha-amylase.

Preferably the mutants of the present invention are secreted into the culture medium during fermentation. Any suitable signal sequence, such as the *aprE* signal peptide, can be used to achieve secretion.

Many of the alpha-amylase mutants of the present invention are useful in formulating various detergent compositions, particularly certain dish care cleaning compositions, especially those cleaning compositions containing known oxidants. Alpha-amylase mutants of the invention can be formulated into known powdered, liquid or gel detergents having pH between 6.5 to 12.0. Suitable granular composition may be made as described in commonly owned US patent applications 07/429,881, 07/533,721 and 07/957,973, all of which are incorporated herein by reference. These detergent cleaning compositions can also contain other enzymes, such as known proteases, lipases, cellulases, endoglycosidases or other amylases, as well as builders, stabilizers or other excipients known to those skilled in the art. These enzymes can be present as co-granules or as blended mixes or in any other manner known to those skilled in

the art. Furthermore, it is contemplated by the present invention that multiple mutants may be useful in cleaning or other applications. For example, a mutant enzyme having changes at both +15 and +197 may exhibit enhanced performance useful in a cleaning product or a multiple mutant comprising changes at +197 and +138 may have improved performance. Specifically preferred mutant enzymes for use in cleaning products, and particularly dish care formulations, include but are not limited to M15T/M197T; M15S/M197T; W138Y/M197T; M15S/W138Y/M197T; and M15T/W138Y/M197T.

Another embodiment of the present invention comprises the combination of the mutant alpha-amylase enzymes described herein in combination with other enzymes (i.e., proteases, lipases, cellulases, etc.), and preferably oxidatively stable proteases. Suitable oxidatively stable proteases include genetically engineered proteases such as those described in US Re 34606, incorporated herein by reference, as well as commercially available enzymes such as DURAZYM (Novo Nordisk), MAXAPEM (Gist-brocades) and PURAFECT OXP (Genencor International, Inc.). Suitable methods for making such protease mutants (oxidatively stable proteases), and particularly such mutants having a substitution for the methionine at a position equivalent to M222 in *B. amyloliquefaciens*, are described in US Re 34606. Suitable methods for determining "equivalent" positions in other subtilisins are provided in Re 34606, EP 257,446 and USSN 212,291, which are incorporated herein by reference.

As described previously, alpha-amylase mutants of the present invention may also be useful in the liquefaction of starch. Starch liquefaction, particularly granular starch slurry liquefaction, is typically carried out at near neutral pH's and high temperatures. As described in commonly owned US applications 07/788,624 and 07/785,623 and US Patent 5,180,669, it appears that an oxidizing agent or inactivating agent of some sort is also present in typical liquefaction processes, which may affect the enzyme activity; thus, in these related patent applications an antioxidant is added to the process to protect the enzyme.

Based on the conditions of a preferred liquefaction process, as described in commonly owned US applications 07/788,624 and 07/785,623 and US Patent 5,180,669, namely low pH, high temperature

and potential oxidation conditions, preferred mutants of the present invention for use in liquefaction processes comprise mutants exhibiting altered pH performance profiles (i.e., low pH profile, pH <6 and preferably pH <5.5), and/or altered thermal stability (i.e., high temperature, about 90°-110°C), and/or altered oxidative stability (i.e., enhanced oxidative stability).

Thus, an improved method for liquefying starch is taught by the present invention, the method comprising liquefying a granular starch slurry from either a wet or dry milling process at a pH from about 4 to 6 by adding an effective amount of an alpha-amylase mutant of the present invention to the starch slurry; optionally adding an effective amount of an antioxidant or other excipient to the slurry; and reacting the slurry for an appropriate time and temperature to liquefy the starch.

The following is presented by way of example and is not to be construed as a limitation to the scope of the claims. Abbreviations used herein, particularly three letter or one letter notations for amino acids are described in Dale, J.W., Molecular Genetics of Bacteria, John Wiley & Sons, (1989) Appendix B.

Experimental

Example 1

Substitutions for the Methionine Residues in

B. licheniformis Alpha-Amylase

The alpha-amylase gene (Fig. 1) was cloned from *B. licheniformis* NCIB8061 obtained from the National Collection of Industrial Bacteria, Aberdeen, Scotland (Gray, G. et al. (1986) J. Bacteriology 166:635-643). The 1.72kb PstI-SstI fragment, encoding the last three residues of the signal sequence; the entire mature protein and the terminator region was subcloned into M13MP18. A synthetic terminator was added between the BclI and SstI sites using a synthetic oligonucleotide cassette of the form:

BclI

SstI

```

5'   GATCAAAACATAAAAAACCGGCCTTGGCCCCGCCGGTTTTTTATTATTTTGTAGCT   3'
3'   TTTTGTATTTTTTGGCCGGAACCGGGGCGGCCAAAAAATAATAAAAC           5'

```

Seq ID No 1

designed to contain the *B. amyloliquefaciens* subtilisin transcriptional terminator (Wells et al. (1983) Nucleic Acid Research 11:7911-7925).

Site-directed mutagenesis by oligonucleotides used essentially the protocol of Zoller, M. et al. (1983) Meth. Enzymol. 100:468-500; briefly, 5'-phosphorylated oligonucleotide primers were used to introduce the desired mutations on the M13 single-stranded DNA template using the oligonucleotides listed in Table I to substitute for each of the seven methionines found in *B. licheniformis* alpha-amylase. Each mutagenic oligonucleotide also introduced a restriction endonuclease site to use as a screen for the linked mutation.

TABLE I
Mutagenic Oligonucleotides for the Substitution of the
Methionine Residues in *B. licheniformis* Alpha-Amylase

M8A	
5'-T GGG ACG CTG <u>GCG CAG TAC TTT</u> GAA TGG T-3'	Seq ID No 2
ScaI+	
M15L	
5'-TG ATG <u>CAG TAC TTT</u> GAA TGG <u>TAC CTG</u> CCC AAT GA-3'	Seq ID No 3
ScaI+ KpnI+	
M197L	
5'-GAT TAT TTG <u>TTG TAT</u> GCC <u>GAT ATC</u> GAC TAT GAC CAT-3'	Seq ID No 4
EcoRV+	
M256A	
5'-CG GGG AAG <u>GAG GCC TTT</u> ACG GTA GCT-3'	Seq ID No 5
StuI+	
M304L	
5'-GC GGC TAT <u>GAC TTA AGG</u> AAA TTG C-3'	Seq ID No 6
AflII+	
M366A	
5'-C TAC GGG <u>GAT GCA TAC</u> GGG ACG A-3'	Seq ID No 7
NsiI+	
M366Y	
5'-C TAC GGG GAT <u>TAC TAC</u> GGG <u>ACC AAG</u> GGA GAC TCC C-3'	Seq ID No 8
StyI+	
M438A	
5'-CC GGT GGG <u>GCC AAG CGG GCC</u> TAT GTT GGC CGG CAA A-3'	Seq ID No 9
SfiI+	

Bold letter indicate base changes introduced by oligonucleotide.

Codon changes indicated in the form M8A, where methionine (M) at position +8 has been changed to alanine (A).

Underlining indicates restriction endonuclease site introduced by oligonucleotide.

The heteroduplex was used to transfect *E. coli* mutL cells (Kramer et al. (1984) Cell 38:879) and, after plaque-purification, clones were analyzed by restriction analysis of the RF1's. Positives were confirmed by dideoxy sequencing (Sanger et al. (1977) Proc. Natl. Acad. Sci. U.S.A. 74:5463-5467) and the PstI-SstI fragments for each subcloned into an *E. coli* vector, plasmid pA4BL.

Plasmid pA4BL

Following the methods described in US application 860,468 (Power et al.), which is incorporated herein by reference, a silent PstI site was introduced at codon +1 (the first amino-acid following the signal cleavage site) of the *aprE* gene from pS168-1 (Stahl, M.L. and Ferrari, E. (1984) J. Bacter. 158:411-418). The *aprE* promoter and signal peptide region was then cloned out of a pJH101 plasmid (Ferrari, F.A. et al. (1983) J. Bacter. 154:1513-1515) as a HindIII-PstI fragment and subcloned into the pUC18-derived plasmid JM102 (Ferrari, E. and Hoch, J.A. (1989) Bacillus, ed. C.R. Harwood, Plenum Pub., pp. 57-72). Addition of the PstI-SstI fragment from *B. licheniformis* alpha-amylase gave pA4BL (Fig. 5) having the resulting *aprE* signal peptide-amylase junction as shown in Fig. 6.

Transformation Into *B. subtilis*

pA4BL is a plasmid able to replicate in *E. coli* and integrate into the *B. subtilis* chromosome. Plasmids containing different variants were transformed into *B. subtilis* (Anagnostopoulos, C. and Spizizen, J. (1961) J. Bacter. 81:741-746) and integrated into the chromosome at the *aprE* locus by a Campbell-type mechanism (Young, M. (1984) J. Gen. Microbiol. 130:1613-1621). The *Bacillus subtilis* strain BG2473 was a derivative of 1168 which had been deleted for amylase (Δ amyE) and two proteases (Δ apr, Δ npr) (Stahl, M.L. and Ferrari, E., J. Bacter. 158:411-418 and US Patent 5,264,366, incorporated herein by reference). After transformation the *sacU32*(Hy) (Henner, D.J. et al. (1988) J. Bacter. 170:296-300) mutation was introduced by PBS-1 mediated transduction (Hoch, J.A. (1983) 154:1513-1515).

N-terminal analysis of the amylase expressed from pA4BL in *B. subtilis* showed it to be processed having four extra alanines at the N-terminus of the secreted amylase protein ("A4 form"). These extra residues had no significant, deleterious effect on the activity or thermal stability of the A4 form and in some applications may enhance performance. In subsequent experiments the correctly processed forms of the *licheniformis* amylase and the variant M197T were made from a very similar construction (see Fig. 6). Specifically, the 5' end of the A4 construction was subcloned on an EcoRI-SstII fragment, from pA4BL (Fig. 5) into M13BM20 (Boehringer

Mannheim) in order to obtain a coding-strand template for the mutagenic oligonucleotide below:

5'-CAT CAG CGT CCC ATT AAG ATT TGC AGC CTG CGC AGA CAT GTT GCT-3'

Seq ID No 10

This primer eliminated the codons for the extra four N-terminal alanines, correct forms being screened for by the absence of the PstI site. Subcloning the EcoRI-SstII fragment back into the pA4BL vector (Fig. 5) gave plasmid pBLapr. The M197T substitution could then be moved, on a SstII-SstI fragment, out of pA4BL (M197T) into the complementary pBLapr vector to give plasmid pBLapr (M197T). N-terminal analysis of the amylase expressed from pBLapr in *B. subtilis* showed it to be processed with the same N-terminus found in *B. licheniformis* alpha-amylase.

Example 2

Oxidative Sensitivity of Methionine Variants

B. licheniformis alpha-amylase, such as Spezyme® AA20 (commercially available from Genencor International, Inc.), is inactivated rapidly in the presence of hydrogen peroxide (Fig. 7). Various methionine variants were expressed in shake-flask cultures of *B. subtilis* and the crude supernatants purified by ammonium sulphate cuts. The amylase was precipitated from a 20% saturated ammonium sulphate supernatant by raising the ammonium sulphate to 70% saturated, and then resuspended. The variants were then exposed to 0.88M hydrogen peroxide at pH 5.0, at 25°C. Variants at six of the methionine positions in *B. licheniformis* alpha-amylase were still subject to oxidation by peroxide while the substitution at position +197 (M197L) showed resistance to peroxide oxidation. (See Fig. 7.) However, subsequent analysis described in further detail below showed that while a variant may be susceptible to oxidation at pH 5.0, 25°C, it may exhibit altered/enhanced properties under different conditions (i.e., liquefaction).

Example 3

Construction of All Possible Variants at Position 197

All of the M197 variants (M197X) were produced in the A4 form by cassette mutagenesis, as outlined in Fig. 8:

M197A
5'-GAT TAT TTG GCG TAT GCC GAT ATC GAC TAT GAC CAT-3'
EcoRV+
ClaI- Seq ID No 11

4) Synthetic primers LAAM14-30 (Table II) were each annealed with the largely complementary common primer LAAM13 (Table II). The resulting cassettes encoded for all the remaining naturally occurring amino acids at position +197 and were ligated, individually, into the vector fragment prepared above.

TABLE II
Synthetic Oligonucleotides Used for Cassette Mutagenesis
to Produce M197X Variants

LAM12	CG GAA GTT TCG AAT GAA AAC G	Seq ID No 12
LAM13	X197bs (EcoRV) GTC GGC ATA TG CAT ATA ATC ATA GTT GCC GTT TTC ATT (BstBI)	Seq ID No 13
LAM14	I197 (BstBI) CG AAT GAA AAC GGC AAC TAT GAT TAT TTG ATC TAT GCC GAC (EcoRV-)	Seq ID No 14
LAM15	F197 (BstBI) CG AAT GAA AAC GGC AAC TAT GAT TAT TTG TTC TAT GCC GAC (EcoRV-)	Seq ID No 15
LAM16	V197 (BstBI) CG AAT GAA AAC GGC AAC TAT GAT TAT TTG GTT TAT GCC GAC (EcoRV-)	Seq ID No 16
LAM17	S197 (BstBI) CG AAT GAA AAC GGC AAC TAT GAT TAT TTG AGC TAT GCC GAC (EcoRV-)	Seq ID No 17
LAM18	P197 (BstBI) CG AAT GAA AAC GGC AAC TAT GAT TAT TTG CCT TAT GCC GAC (EcoRV-)	Seq ID No 18
LAM19	T197 (BstBI) CG AAT GAA AAC GGC AAC TAT GAT TAT TTG ACA TAT GCC GAC (EcoRV-)	Seq ID No 19
LAM20	Y197 (BstBI) CG AAT GAA AAC GGC AAC TAT GAT TAT TTG TAC TAT GCC GAC (EcoRV-)	Seq ID No 20
LAM21	H197 (BstBI) CG AAT GAA AAC GGC AAC TAT GAT TAT TTG CAC TAT GCC GAC (EcoRV-)	Seq ID No 21
LAM22	G197 (BstBI) CG AAT GAA AAC GGC AAC TAT GAT TAT TTG GGC TAT GCC GAC (EcoRV-)	Seq ID No 22

LAAM23	Q197 (BstBI)	CG AAT GAA AAC GGC AAC TAT GAT TAT TTG CAA TAT GCC GAC (EcorV-)	Seq ID No 23
LAAM24	N197 (BstBI)	CG AAT GAA AAC GGC AAC TAT GAT TAT TTG AAC TAT GCC GAC (EcorV-)	Seq ID No 24
LAAM25	K197 (BstBI)	CG AAT GAA AAC GGC AAC TAT GAT TAT TTG AAA TAT GCC GAC (EcorV-)	Seq ID No 25
LAAM26	D197 (BstBI)	CG AAT GAA AAC GGC AAC TAT GAT TAT TTG GAT TAT GCC GAC (EcorV-)	Seq ID No 26
LAAM27	E197 (BstBI)	CG AAT GAA AAC GGC AAC TAT GAT TAT TTG GAA TAT GCC GAC (EcorV-)	Seq ID No 27
LAAM28	C197 (BstBI)	CG AAT GAA AAC GGC AAC TAT GAT TAT TTG TGT TAT GCC GAC (EcorV-)	Seq ID No 28
LAAM29	W197 (BstBI)	CG AAT GAA AAC GGC AAC TAT GAT TAT TTG TGG TAT GCC GAC (EcorV-)	Seq ID No 29
LAAM30	R197 (BstBI)	CG AAT GAA AAC GGC AAC TAT GAT TAT TTG AGA TAT GCC GAC (EcorV-)	Seq ID No 30

The cassettes were designed to destroy the EcoRV site upon ligation, thus plasmids from *E. coli* transformants were screened for loss of this unique site. In addition, the common bottom strand of the cassette contained a frame-shift and encoded a NsiI site, thus transformants derived from this strand could be eliminated by screening for the presence of the unique NsiI site and would not be expected, in any case, to lead to expression of active amylase.

Positives by restriction analysis were confirmed by sequencing and transformed in *B. subtilis* for expression in shake-flask cultures (Fig. 9). The specific activity of certain of the M197X mutants was then determined using a soluble substrate assay. The data generated using the following assay methods are presented below in Table III.

Soluble Substrate Assay: A rate assay was developed based on an end-point assay kit supplied by Megazyme (Aust.) Pty. Ltd.: Each vial of substrate (p-nitrophenyl maltoheptaoside, BPNPG7) was dissolved in 10ml of sterile water, followed by a 1 to 4 dilution in assay buffer (50mM maleate buffer, pH 6.7, 5mM calcium chloride, 0.002% Tween20). Assays were performed by adding 10 μ l of amylase to 790 μ l of the substrate in a cuvette at 25°C. Rates of hydrolysis were measured as the rate of change of absorbance at 410nm, after a delay of 75 seconds. The assay was linear up to rates of 0.4 absorption units/min.

The amylase protein concentration was measured using the standard Bio-Rad assay (Bio-Rad Laboratories) based on the method of Bradford, M. (1976) Anal. Biochem. 72:248) using bovine serum albumin standards.

Starch Hydrolysis Assay: The standard method for assaying the alpha-amylase activity of Spezyme® AA20 was used. This method is described in detail in Example 1 of USSN 07/785,624, incorporated herein by reference. Native starch forms a blue color with iodine but fails to do so when it is hydrolyzed into shorter dextrin molecules. The substrate is soluble Lintner starch 5gm/liter in phosphate buffer, pH 6.2 (42.5gm/liter potassium dihydrogen phosphate, 3.16gm/liter sodium hydroxide). The sample is added in 25mM calcium chloride and activity is measured as the time taken to give a negative iodine test upon incubation at 30°C. Activity is

recorded in liquefons per gram or ml (LU) calculated according to the formula:

$$\text{LU/ml or LU/g} = \frac{570}{V \times t} \times D$$

Where LU=liquefon unit

V=volume of sample (5ml)

t=dextrinization time (minutes)

D=dilution factor=dilution volume/ml or g of added enzyme.

TABLE III

<u>ALPHA-AMYLASE</u>	<u>SPECIFIC ACTIVITY (as % of AA20 value) on:</u>	
	<u>Soluble Substrate</u>	<u>Starch</u>
Spezyme® AA20	100	100
A4 form	105	115
M15L (A4 form)	93	94
M15L	85	103
M197T (A4 form)	75	83
M197T	62	81
M197A (A4 form)	88	89
M197C	85	85
M197L (A4 form)	51	17

Example 4

Characterization of Variant M15L

Variant M15L made as per the prior examples did not show increased amylase activity (Table III) and was still inactivated by hydrogen peroxide (Fig. 7). It did, however, show significantly increased performance in jet-liquefaction of starch, especially at low pH as shown in Table IV below.

Starch liquefaction was typically performed using a Hydroheater M 103-M steam jet equipped with a 2.5 liter delay coil behind the mixing chamber and a terminal back pressure valve. Starch was fed to the jet by a Moyno pump and steam was supplied by a 150 psi steam line, reduced to 90-100 psi. Temperature probes were installed just after the Hydroheater jet and just before the back pressure valve.

Starch slurry was obtained from a corn wet miller and used within two days. The starch was diluted to the desired solids level with deionized water and the pH of the starch was adjusted with 2% NaOH or saturated Na_2CO_3 . Typical liquefaction conditions were:

Starch	32%-35% solids
Calcium	40-50 ppm (30 ppm add d)
pH	5.0-6.0
Alpha-amylase	12-14 LU/g starch dry basis

Starch was introduced into the jet at about 350 ml/min. The jet temperature was held at 105°-107°C. Samples of starch were transferred from the jet cooker to a 95°C second stage liquefaction and held for 90 minutes.

The degree of starch liquefaction was measured immediately after the second stage liquefaction by determining the dextrose equivalence (DE) of the sample and by testing for the presence of raw starch, both according to the methods described in the Standard Analytical Methods of the Member Companies of the Corn Refiners Association, Inc., sixth edition. Starch, when treated generally under the conditions given above and at pH 6.0, will yield a liquefied starch with a DE of about 10 and with no raw starch. Results of starch liquefaction tests using mutants of the present invention are provided in Table IV.

TABLE IV

Performance of Variants M15L (A4 form) and M15L in Starch Liquefaction

	<u>pH</u>	<u>DE after 90 Mins.</u>
Spezyme® AA20	5.9	9.9
M15L (A4 form)	5.9	10.4
Spezyme® AA20	5.2	1.2
M15L (A4 form)	5.2	2.2
Spezyme® AA20	5.9	9.3*
M15L	5.9	11.3*
Spezyme® AA20	5.5	3.25**
M15L	5.5	6.7**
Spezyme® AA20	5.2	0.7**
M15L	5.2	3.65**

* average of three experiments

** average of two experiments

Example 5

Construction of M15X Variants

Following generally the processes described in Example 3 above, all variants at M15 (M15X) were produced in *nativ B. licheniformis* by cassette mutagenesis, as outlined in Fig. 12:

1) Site directed mutagenesis (via primer extension in M13) was used to introduce unique restriction sites flanking the M15 codon to facilitate insertion of a mutagenesis cassette. Specifically, a BstB1 site at codons 11-13 and a MscI site at codons 18-20 were introduced using the two oligonucleotides shown below:

M15XBstB1 5'-G ATG CAG TAT TTC GAA CTGG TAT A-3'
BstB1 Seq ID No 48

M15XMscI 5'-TG CCC AAT GAT GGC CAA CAT TGG AAG-3'
MscI Seq ID No 49

2) The vector for M15X cassette mutagenesis was then constructed by subcloning the SfiI-SstII fragment from the mutagenized amylase (BstB1+, MscI+) into plasmid pBLapr. The resulting plasmid was then digested with BstB1 and MscI and the large vector fragment isolated by electroelution from a polyacrylamide gel.

3) Mutagenesis cassettes were created as with the M197X variants. Synthetic oligomers, each encoding a substitution at codon 15, were annealed to a common bottom primer. Upon proper ligation of the cassette to the vector, the MscI is destroyed allowing for screening of positive transformants by loss of this site. The bottom primer contains an unique SnaB1 site allowing for the transformants derived from the bottom strand to be eliminated by screening for the SnaB1 site. This primer also contains a frameshift which would also eliminate amylase expression for the mutants derived from the common bottom strand.

The synthetic cassettes are listed in Table V and the general cassette mutagenesis strategy is illustrated in Figure 12.

TABLE V
Synthetic Oligonucleotides Used for Cassette Mutagenesis
to Produce M15X Variants

M15A	(BstB1)	C	GAA	TGG	TAT	<u>GCT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 50
M15R	(BstB1)	C	GAA	TGG	TAT	<u>CGC</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 51
M15N	(BstB1)	C	GAA	TGG	TAT	<u>AAT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 52
M15D	(BstB1)	C	GAA	TGG	TAT	<u>GAT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 53
M15H	(BstB1)	C	GAA	TGG	TAT	<u>CAC</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 54
M15K	(BstB1)	C	GAA	TGG	TAT	<u>AAA</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 55
M15P	(BstB1)	C	GAA	TGG	TAT	<u>CCG</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 56
M15S	(BstB1)	C	GAA	TGG	TAT	<u>TCT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 57
M15T	(BstB1)	C	GAA	TGG	TAC	<u>ACT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 58
M15V	(BstB1)	C	GAA	TGG	TAT	<u>GTT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 59
M15C	(BstB1)	C	GAA	TGG	TAT	<u>TGT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 60
M15Q	(BstB1)	C	GAA	TGG	TAT	<u>CAA</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 61
M15E	(BstB1)	C	GAA	TGG	TAT	<u>GAA</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 62
M15G	(BstB1)	C	GAA	TGG	TAT	<u>GGT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 63
M15I	(BstB1)	C	GAA	TGG	TAT	<u>ATT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 64
M15F	(BstB1)	C	GAA	TGG	TAT	<u>TTT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 65
M15W	(BstB1)	C	GAA	TGG	TAC	<u>TGG</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 66
M15Y	(BstB1)	C	GAA	TGG	TAT	<u>TAT</u>	CCC	AAT	GAC	GG	(Msc1)	Seq ID No 67
M15X	(Msc1)	CC	GTC	ATT	GGG	ACT	ACG	TAC	CAT	T	(BstB1)	Seq ID No 68
(bottom strand)												

Underline indicates codon changes at amino acid position 15.

Conservative substitutions were made in some cases to prevent introduction of new restriction sites.

Example 6

Bench Liquefaction with M15X Variants

El ven alpha-amylase variants with substitutions for M15 made as per Example 5 were assayed for activity, as compared to Spezyme® AA20

(commercially available from Genencor International, Inc.) in liquefaction at pH 5.5 using a bench liquefaction system. The bench scale liquefaction system consisted of a stainless steel coil (0.25 inch diameter, approximately 350 ml volume) equipped with a 7 inch long static mixing element approximately 12 inches from the anterior end and a 30 psi back pressure valve at the posterior end. The coil, except for each end, was immersed in a glycerol-water bath equipped with thermostatically controlled heating elements that maintained the bath at 105-106°C.

Starch slurry containing enzyme, maintained in suspension by stirring, was introduced into the reaction coil by a piston driven metering pump at about 70 ml/min. The starch was recovered from the end of the coil and was transferred to the secondary hold (95°C for 90 minutes). Immediately after the secondary hold, the DE of the liquefied starch was determined, as described in Example 4. The results are shown in Fig. 16.

Example 7

Characterization of M197X Variants

As can be seen in Fig. 9, there was a wide range of amylase activity (measured in the soluble substrate assay) expressed by the M197X (A4 form) variants. The amylases were partially purified from the supernatants by precipitation with two volumes of ethanol and resuspension. They were then screened for thermal stability (Fig. 10) by heating at 95°C for 5 minutes in 10mM acetate buffer pH 5.0, in the presence of 5mM calcium chloride; the A4 wild-type retained 28% of its activity after incubation. For M197W and M197P we were unable to recover active protein from the supernatants. Upon sequencing, the M197H variant was found to contain a second mutation, N190K. M197L was examined in a separate experiment and was one of the lowest thermally stable variants. There appears to be a broad correlation between expression of amylase activity and thermal stability. The *licheniformis* amylase is restricted in what residues it can accommodate at position 197 in terms of retaining or enhancing thermal stability: cysteine and threonine are preferred for maximal thermal stability under these conditions whereas alanine and isoleucine are of intermediate stability. However, other substitutions at position +197 result in lowered thermal stability which may be useful for other applications. Additionally, different substitutions at +197 may have other beneficial properties, such as

altered pH performance profile or altered oxidative stability. For example, the M197C variant was found to inactivate readily by air oxidation but had enhanced thermal stability. Conversely, compared to the M197L variant, both M197T and M197A retained not only high thermal stability (Fig. 10), but also high activity (Table III), while maintaining resistance to inactivation by peroxide at pH 5 to pH 10 (Fig. 7).

Example 8

Stability and Performance in Detergent Formulation

The stability of the M197T (A4 form), M197T and M197A (A4 form) was measured in automatic dish care detergent (ADD) matrices. 2ppm Savinase™ (a protease, commercially available from Novo Industries, of the type commonly used in ADD) were added to two commercially available bleach-containing ADD's: Cascade™ (Procter and Gamble, Ltd.) and Sunlight™ (Unilever) and the time course of inactivation of the amylase variants and Termamyl™ (a thermally stable alpha-amylase available from Novo Nordisk, A/S) followed at 65°C. The concentration of ADD product used in both cases was equivalent to 'pre-soak' conditions: 14gm product per liter of water (7 grams per gallon hardness). As can be seen (Figs. 11a and 11b), both forms of the M197T variant were much more stable than Termamyl™ and M197A (A4 form), which were inactivated before the first assay could be performed. This stability benefit was seen in the presence or absence of starch as determined by the following protocol. Amylases were added to 5ml of ADD and Savinase™, prewarmed in a test tube and, after vortexing, activities were assayed as a function of time, using the soluble substrate assay. The "+ starch" tube had spaghetti starch baked onto the sides (140°C, 60 mins.). The results are shown in Figs. 11a and 11b.

Example 9

Characterization of M15X Variants

All M15X variants were propagated in *Bacillus subtilis* and the expression level monitored as shown in Fig. 13. The amylase was isolated and partially purified by a 20-70% ammonium sulfate cut. The specific activity of these variants on the soluble substrate was determined as per Example 3 (Fig. 14). Many of the M15X amylases have specific activities greater than that of Spezyme® AA20. A benchtop heat stability assay was performed on the variants by heating the amylase at 90°C for 5 min. in 50 mM acetate buffer pH 5

in the presence of 5 mM CaCl₂ (Fig. 15). Most of the variants performed as well as Spezyme® AA20 in this assay. Those variants that exhibited reasonable stability in this assay (reasonable stability defined as those that retained at least about 60% of Spezyme® AA20's heat stability) were tested for specific activity on starch and for liquefaction performance at pH 5.5. The most interesting of those mutants are shown in Fig. 16. M15D, N and T, along with L, outperformed Spezyme® AA20 in liquefaction at pH 5.5 and have increased specific activities in both the soluble substrate and starch hydrolysis assays.

Generally, we have found that by substituting for the methionine at position 15, we can provide variants with increased low pH-liquefaction performance and/or increased specific activity.

Example 10

Tryptophan Sensitivity to Oxidation

Chloramine-T (sodium N-chloro-p-toluenesulfonimide) is a selective oxidant, which oxidizes methionine to methionine sulfoxide at neutral or alkaline pH. At acidic pH, chloramine-T will modify both methionine and tryptophan (Schechter, Y., Burstein, Y. and Patchornik, A. (1975) *Biochemistry* 14 (20) 4497-4503). Fig. 17 shows the inactivation of *B. licheniformis* alpha-amylase with chloramine-T at pH 8.0 (AA20 = 0.65 mg/ml, M197A = 1.7 mg/ml, M197L = 1.7 mg/ml). The data shows that by changing the methionine at position 197 to leucine or alanine, the inactivation of alpha-amylase can be prevented. Conversely, as shown in Fig. 18, at pH 4.0 inactivation of the M197A and M197L proceeds, but require more equivalents of chloramine-T (Fig. 18; AA20 = 0.22 mg/ml, M197A = 4.3 mg/ml, M197L = 0.53 mg/ml; 200 mM NaAcetate at pH 4.0). This suggests that a tryptophan residue is also implicated in the chloramine-T mediated inactivation event. Furthermore, tryptic mapping and subsequent amino acid sequencing indicated that the tryptophan at position 138 was oxidized by chloramine-T (data not shown). To prove this, site-directed mutants were made at tryptophan 138 as provided below:

Preparation of Alpha-Amylase Double Mutants W138 and M197

Certain variants of W138 (F, Y and A) were made as double mutants, with M197T (made as per the disclosure of Example 3). The double mutants were made following the methods described in Examples 1 and

3. Generally, single negative strands of DNA were prepared from an M13MP18 clone of the 1.72kb coding sequence (Pst I-Sst I) of the *B. licheniformis* alpha-amylase M197T mutant. Site-directed mutagenesis was done using the primers listed below, essentially by the method of Zoller, M. et al. (1983) except T4 gene 32 protein and T4 polymerase were substituted for Klenow. The primers all contained unique sites, as well as the desired mutation, in order to identify those clones with the appropriate mutation.

Tryptophan 138 to Phenylalanine

133 134 135 136 137 138 139 140 141 142 143
CAC CTA ATT AAA GCT TTC ACA CAT TTT CAT TTT
Hind III

Seq ID No 42

Tryptophan 138 to Tyrosine

133 134 135 136 137 138 139 140 141 142 143
CAC CTA ATT AAA GCT TAC ACA CAT TTT CAT TTT
Hind III

Seq ID No 43

Tryptophan 138 to Alanine - This primer also engineers unique sites upstream and downstream of the 138 position.

127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142
C CGC GTA ATT TCC GGA GAA CAC CTA ATT AAA GCC GCA ACA CAT TTT CAT
BspE I

143 144 145 146 147
TTT CCC GGG CGC GGC AG
Xma I

Seq ID No 44

Mutants were identified by restriction analysis and W138F and W138Y confirmed by DNA sequencing. The W138A sequence revealed a nucleotide deletion between the unique BspE I and Xma I sites, however, the rest of the gene sequenced correctly. The 1.37kb SstII/SstI fragment containing both W138X and M197T mutations was moved from M13MP18 into the expression vector pBLapr resulting in pBLapr (W138F, M197T) and pBLapr (W138Y, M197T). The fragment containing unique BspE I and Xma I sites was cloned into pBLapr (BspE I, Xma I, M197T) since it is useful for cloning cassettes containing other amino acid substitutions at position 138.

Single Mutations at Amino Acid Position 138

Following the general methods described in the prior examples, certain single variants of W138 (F, Y, L, H and C) were made.

The 1.24kb Asp718-SstI fragment containing the M197T mutation in plasmid pBLapr (W138X, M197T) of Example 7 was replaced by the wild-type fragment with methionine at 197, resulting in pBLapr (W138F), pBLapr (W138Y) and pBLapr (BspE I, Xma I).

The mutants W138L, W138H and W138C were made by ligating synthetic cassettes into the pBLapr (BspE I, Xma I) vector using the following primers:

Tryptophan 138 to Leucine

CC GGA GAA CAC CTA ATT AAA GCC CTA ACA CAT TTT CAT TTT C

Seq ID No 45

Tryptophan 138 to Histidine

CC GGA GAA CAC CTA ATT AAA GCC CAC ACA CAT TTT CAT TTT C

Seq ID No 46

Tryptophan 138 to Cysteine

CC GGA GAA CAC CTA ATT AAA GCC TGC ACA CAT TTT CAT TTT C

Seq ID No 47

Reaction of the double mutants M197T/W138F and M197T/W138Y with chloramine-T was compared with wild-type (AA20 = 0.75 mg/ml, M197T/W138F = 0.64 mg/ml, M197T/W138Y = 0.60 mg/ml; 50 mM NaAcetate at pH 5.0). The results shown in Fig. 19 show that mutagenesis of tryptophan 138 has caused the variant to be more resistant to chloramine-T.

Example 11

Preparation of Multiple Mutants

Following the methods of Examples 1, 3, 5 and 10, the following multiple mutants were made: M15T/M197T; M15S/M197T; W138Y/M197T; M15S/W138Y/M197T and M15T/W138Y/M197T. Certain of these multiple mutants were previously exemplified, for example, W138Y/M197T was made and tested in Example 10. The multiple mutants were identified by restriction analysis.

Various multiple mutants within the scope of the present invention were further tested for performance as cleaning products (automatic dish care detergent) additives. These mutants are detailed below.

Stability Testing

A 4000 ppm solution of automatic dishwashing detergent (ADD) containing perborate and TAED was prepared in water with a hardness of 7 gpg. Certain amylase mutants described above were added to this ADD solution to yield a rate of 0.4 when assayed by the Ceralpha method (Megazyme (Austr.) Pty. Ltd., Parramatta, NSW, Australia). One set of samples was held at room temperature (21-23°C) for about 30 min. (non-heated). A second set of samples was warmed from room temperature to about 65°C after addition of the enzyme (heated). 30 min. after addition of the enzyme, the activity of the amylase mutants was measured and the activity relative to the activity at the time of addition of the enzyme was calculated (relative activity %).

The results shown in Fig. 20 indicate that the methionine at position +197 of *B. licheniformis* alpha-amylase should be modified for stability in a formulation comprising ADD + perborate + TAED.

Starch Hydrolysis Assay

A 4000 ppm solution of automatic dishwashing detergent (ADD) containing perborate and TAED was prepared in water with a hardness of 7 gpg and three cooked pieces of elbow macaroni were added. The amylase mutants described above were added to this ADD solution to yield a final concentration of 5 ppm active enzyme. The tubes were incubated at 50°C for about 30 min. and the concentration of reducing sugars released was measured against a glucose standard curve using the dinitrosalicylic acid method. Results are shown in Table VI.

Table VI

Enzyme	Reducing Sugar Concentration (g/l)	Standard Deviation
No Enzyme	1.64	0.12
Wild-Type	4.97	0.30
M15S/M197T	5.40	0.36
M15T/M197T	5.85	0.38
W138Y/M197T	6.48	0.36
M15S/W138Y/M197T	6.04	0.74
M15T/W138Y/M197T	6.27	0.49

The results shown in Table VI show that M15T/M197T; M15S/M197T; W138Y/M197T; M15S/W138Y/M197T and M15T/W138Y/M197T performed well compared to no enzyme and wild-type alpha-amylase controls.

Oatmeal Stains

Dishes were evenly soiled with a cooked, blended oatmeal paste and dried overnight at 37°C. Dishes were loaded in an ASKO Model 770 dishwasher and washed at 45°C on the Quick Wash cycle using 10 g of automatic dishwashing detergent containing 5% perborate, 3% TAED and 11 mg of certain amylase enzyme(s). The plates were weighed before soiling, after soiling and after washing, and the average % soil removed from all plates was calculated. The data are shown below in Table VII.

Table VII

Enzyme	% Soil Removed (Average of All Dishes)
Wild-Type	61
M15S/M197T	66
M15T/M197T	71
W138Y/M197T	68
M15S/W138Y/M197T	62
M15T/W138Y/M197T	72

The data show that the mutant enzymes provided a benefit greater than that provided by the wild-type. Wild-type amylase provided a 20% greater cleaning benefit in removing oatmeal than did ADD without amylase.

Example 12

Dish Care Cleaning Composition

1% (w/w) granules of wild-type and mutant amylases were formulated with a Korex Automatic Dishwasher Detergent to which 5% (w/w) sodium perborate monohydrate and 3% (w/w) TAED were added. Samples of these formulations were placed at room temperature (21-23°C) or at 38°C and 80% relative humidity for four weeks. Results are shown in Figs. 21 and 22.

The data show that the wild-type amylase activity, as measured by the Ceralpha method, decreased with increasing storage time in detergent. At room temperature, the mutant enzymes were completely stable. At 38°C and 80% relative humidity, all mutants were more stable than the wild-type.

The advantage of formulating an automatic dishwashing detergent with these mutant amylases is that these mutants are significantly more stable than the wild-type in the presence of perborate and TAED and they provide a significant performance benefit in removing starchy food stains in the wash.

Example 13

Oxidatively Stable Protease/Oxidatively Stable Amylase

Stability Studies

Enzyme granules containing either: 1) wild-type protease and wild-type amylase; or 2) bleach stable protease (GG36-M222S) made by the methods described in US Re 34606 and bleach stable amylase (AA20-M15T/W138Y/M197T) were dissolved in buffer containing 0.1 M sodium borate pH 10.2 and 0.005% Tween 80 at a concentration of 12.5 mg of each enzyme. To 9 ml of these solutions was added either 1 ml distilled water or 1 ml 30% hydrogen peroxide. After incubation of the solutions at 25°C for 30 minutes, the protease and amylase activity in each solution was measured and is reported as % of the original activity. The data are shown below in Table VIII.

Table VIII

Treatment	Enzyme	% Activity After 30 Min
Water	WT Amylase	104
Water	WT Protease	94
Water	M222S Protease	119
Water	TYT Amylase	88
3% Peroxide	WT Amylase	14
3% Peroxide	WT Protease	7
3% Peroxide	M222S Protease	116
3% Peroxide	TYT Amylase	75

The data show that the combination of a bleach-stable amylase mutant and a bleach-stable protease mutant, both with mutations at amino acid residues sensitive to oxidation, provides the combined benefits of protease and amylase in a formulation resistant to inactivation by bleach. The combination of a bleach-stable amylase and a bleach-stable protease retains most of its initial activity after 30 minutes in bleach, while the combination of wild-type enzymes loses over 80% of its initial activity in the same period of time.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Barnett, Christopher
Mitchinson, Colin
Power, Scott D.
- (ii) TITLE OF INVENTION: An Improved Cleaning Composition
- (iii) NUMBER OF SEQUENCES: 68
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genencor International
 - (B) STREET: 180 Kimball Way
 - (C) CITY: South San Francisco
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Horn, Margaret A.
 - (B) REGISTRATION NUMBER: 33,401
 - (C) REFERENCE/DOCKET NUMBER: GC220-3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 742-7536
 - (B) TELEFAX: (415) 742-7217

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCAAAACA TAAAAAACCG GCCTTGGCCC CGCCGGTTTT TTATTATTTT TGAGCT

56

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGGGACGCTG GCCCACTACT TTGAATGGT

29

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGATGCAGTA CTTTGAATGG TACCTGCCCA ATGA

34

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATTATTTGT TGTATGCCGA TATCGACTAT GACCAT

36

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs.
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGGAAGGA GGCCTTTACG GTAGCT

26

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGCTATGA CTTAAGGAAA TTGC

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (gen mic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
CTACGGGGAT GCATACGGGA CGA 23
- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
CTACGGGGAT TACTACGGGA CCAAGGGAGA CTCCC 35
- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
CCGGTGGGGC CAAGCGGGCC TATGTTGGCC GGCAAA 36
- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
CATCAGCGTC CCATTAAGAT TTGCAGCCTG CGCAGACATG TTGCT 45
- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
GATTATTGG CGTATGCCGA TATCGACTAT GACCAT 36
- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAAGTTTC GAATGAAAAC G

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGGCATAT GCATATAATC ATAGTTGCCG TTTTCATT

38

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGAATGAAAA CGGCAACTAT GATTATTTGA TCTATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGAATGAAAA CGGCAACTAT GATTATTTGT TCTATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGAATGAAAA CGGCAACTAT GATTATTTGC TTTATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGAATGAAAA CGGCAACTAT GATTATTTGA GCTATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGAATGAAAA CGGCAACTAT GATTATTTGC CTTATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGAATGAAAA CGGCAACTAT GATTATTTGA CATATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGAATGAAAA CGGCAACTAT GATTATTTGT ACTATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
CGAATGAAAA CGGCAACTAT GATTATTTGC ACTATGCCGA C 41
- (2) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
CGAATGAAAA CGGCAACTAT GATTATTTGG GCTATGCCGA C 41
- (2) INFORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
CGAATGAAAA CGGCAACTAT GATTATTTGC AATATGCCGA C 41
- (2) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
CGAATGAAAA CGGCAACTAT GATTATTTGA ACTATGCCGA C 41
- (2) INFORMATION FOR SEQ ID NO:25:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
GCAATGAAAA CGGCAACTAT GATTATTTGA AATATGCCGA C 41
- (2) INFORMATION FOR SEQ ID NO:26:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: singl
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGAATGAAAA CGGCAACTAT GATTATTTGG ATTATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGAATGAAAA CGGCAACTAT GATTATTTGG AATATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGAATGAAAA CGGCAACTAT GATTATTTGT GTATTGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGAATGAAAA CGGCAACTAT GATTATTTGT GGTATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGAATGAAAA CGGCAACTAT GATTATTTGA GATATGCCGA C

41

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1968 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

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AGCTTGAAGA AGTGAAGAAG CAGAGAGGCT ATTGAATAAA TGAGTAGAAA GCGCCATATC      60
GGCGCTTTTC TTTTGGGAAGA AAATATAGGG AAAATGGTAC TTGTTAAAAA TTCGGAATAT      120
TTATACAACA TCATATGTTT CACATTGAAA GGGGAGGAGA ATCATGAAAC AACAAAAACG      180
GCTTTACGCC CGATTGCTGA CGCTGTTATT TCGGCTCATC TTCTTGCTGC CTCATTCTGC      240
AGCAGCGGCG GCAAATCTTA ATGGGACGCT GATGCAGTAT TTTGAATGGT ACATGCCCAA      300
TGACGGCCAA CATTGGAAGC GTTTGCAAAA CGACTCGGCA TATTTGGCTG AACACGGTAT      360
TACTGCCGTC TGGATTCCCC CGGCATATAA GGGAACGAGC CAAGCGGATG TGGGCTACGG      420
TGCTTACGAC CTTTATGATT TAGGGGAGTT TCATCAAAAA GGGACGGTTC GGACAAAGTA      480
CGGCACAAAA GGAGAGCTGC AATCTGCGAT CAAAAGTCTT CATTCGCCG ACATTAACGT      540
TTACGGGGAT GTGGTCATCA ACCACAAAGG CGGCGTGAT GCGACCGAAG ATGTAACCGC      600
GGTTGAAGTC GATCCCGCTG ACCGCAACCG CGTAATTTC AAGAGAACACC TAATTAAGC      660
CTGGACACAT TTTCAATTTT CCGGGCGCGG CAGCACATAC AGCGATTTTA AATGGCATTG      720
GTACCATTTT GACCGAACCG ATTGGGACGA GTCCCGAAAG CTGAACCGCA TCTATAAGTT      780
TCAAGGAAAG GCTTGGGATT GGGAGTTTC CAATGAAAC GGCAACTATG ATTATTTGAT      840
GTATGCCGAC ATCGATTATG ACCATCCTGA TGTCCGAGCA GAAATTAAGA GATGGGGCAC      900
TTGGTATGCC AATGAACTGC AATTGGACGG TTTCCGTCTT GATGCTGTCA AACACATTAA      960
ATTTTCTTTT TTGCGGGATT GGGTTAATCA TGTACGGAA AAAACGGGGA AGGAAATGTT     1020
TACGGTAGCT GAATATTGGC AGAATGACTT GGGCGCGCTG GAAACTATT TGAACAAAC     1080
AAATTTTAAT CATTCAGTGT TTGACGTGCC GCTTCATTAT CAGTTCCATG CTGCATCGAC     1140
ACAGGGAGGC GGCTATGATA TGAGGAAATT GCTGAACGGT ACGGTCGTTT CCAAGCATCC     1200
GTTGAAATCG GTTACATTG TCGATAACCA TGATACACAG CCGGGGCAAT CGCTTGAGTC     1260
GACTGTCCAA ACATGGTTTA AGCCGCTTGC TTACGCTTTT ATTCTCACA GGAATCTGG     1320
ATACCCCTCAG GTTTTCTACG GGGATATGTA CCGGACGAAA GGAGACTCCC AGCGCGAAAT     1380
TCCTGCCTTG AAACACAAAA TTGAACCGAT CTTAAAAGCG AGAAAACAGT ATGCGTACGG     1440
AGCACAGCAT GATTATTTTC ACCACCATGA CATTGTCCGC TGGACAAGGG AAGGCGACAG     1500
CTCGGTTGCA AATTCAGGTT TGGCGGCATT AATAACAGAC GGACCCGGTG GGGCAAACGG     1560
AATGTATGTC GGCCGGCAAA ACGCCGGTGA GACATGGCAT GACATTACCG GAAACCGTTC     1620
GGAGCCGGTT GTCATCAATT CGGAAGGCTG GGGAGAGTTT CACGTAAACG GCGGGTCGGT     1680
TTCAATTTAT GTTCAAAGAT AGAAGAGCAG AGAGGACGGA TTCTCTGAAG GAAATCCGTT     1740
TTTTATTTT GCCCGTCTTA TAAATTTCTT TGATTACATT TTATAATTAA TTTTAACAAA     1800

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GTGTCATCAG CCCTCAGGAA GGACTTGCTG ACAGTTTGAA TCGCATAGGT AAGGCGGGGA 1860
 TGAATGGCA ACOTTATCTG ATGTAGCAAA GAAAGCAAAT GTGTCGAAAA TGACGGTATC 1920
 GCGGGTGATC AATCATCCTG AGACTGTGAC GGATGAATTG AAAAAGCT 1968

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15
 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu
 20 25 30
 Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45
 Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60
 Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80
 Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
 85 90 95
 Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
 100 105 110
 Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
 115 120 125
 Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
 130 135 140
 Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160
 Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175
 Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205
 Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220
 Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240
 Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
 245 250 255
 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
 260 265 270
 Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
 290 295 300
 Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335
 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350
 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365
 Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380
 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 385 390 395 400
 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415
 Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430
 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480
 Val Gln Arg

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 511 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe
 1 5 10 15
 Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Ala Asn Leu
 20 25 30
 Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro Asn Asp Gly
 35 40 45
 His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu Ala Glu His Gly
 50 55 60
 Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln Ala
 65 70 75 80
 Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe His
 85 90 95
 Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu Gln
 100 105 110

Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly Asp
 115 120 125
 Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp Val Thr
 130 135 140
 Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly Glu
 145 150 155 160
 His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly Ser
 165 170 175
 Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Thr Asp
 180 185 190
 Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln Gly Lys
 195 200 205
 Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp Tyr Leu
 210 215 220
 Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala Glu Ile
 225 230 235 240
 Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp Gly Phe
 245 250 255
 Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg Asp Trp
 260 265 270
 Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr Val Ala
 275 280 285
 Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn Lys
 290 295 300
 Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln Phe
 305 310 315 320
 His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys Leu Leu
 325 330 335
 Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser Val Thr Phe Val
 340 345 350
 Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val Gln
 355 360 365
 Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu Ser
 370 375 380
 Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly Asp
 385 390 395 400
 Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile Leu
 405 410 415
 Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe Asp
 420 425 430
 His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val Ala
 435 440 445
 Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala Lys
 450 455 460
 Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp Ile
 465 470 475 480
 Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly Trp Gly
 485 490 495
 Glu Phe His Val Asn Gly Gly Ser Val Ser Il Tyr Val Gln Arg
 500 505 510

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

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Met Arg Gly Arg Gly Asn Met Ile Gln Lys Arg Lys Arg Thr Val Ser
 1           5           10           15
Phe Arg Leu Val Leu Met Cys Thr Leu Leu Phe Val Ser Leu Pro Ile
          20           25           30
Thr Lys Thr Ser Ala Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp
          35           40           45
Tyr Thr Pro Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala
          50           55           60
Glu His Leu Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala
          65           70           75           80
Tyr Lys Gly Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu
          85           90           95
Tyr Asp Leu Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr
          100          105          110
Gly Thr Lys Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg
          115          120          125
Asn Val Gln Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala
          130          135          140
Asp Ala Thr Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg
          145          150          155          160
Asn Gln Glu Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe
          165          170          175
Arg Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp
          180          185          190
Tyr His Phe Asp Gly Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg
          195          200          205
Ile Phe Lys Phe Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser
          210          215          220
Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr
          225          230          235          240
Asp His Pro Asp Val Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr
          245          250          255
Ala Asn Glu Leu Ser Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His
          260          265          270
Ile Lys Phe Ser Phe Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala
          275          280          285
Thr Gly Lys Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala
          290          295          300
Gly Lys Leu Glu Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val
          305          310          315          320

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Phe Asp Val Pro Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly
 325 330 335
 Gly Gly Tyr Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg
 340 345 350
 His Pro Glu Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro
 355 360 365
 Gly Gln Ser Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala
 370 375 380
 Tyr Ala Phe Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr
 385 390 395 400
 Gly Asp Met Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser
 405 410 415
 Leu Lys Asp Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala
 420 425 430
 Tyr Gly Pro Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp
 435 440 445
 Thr Arg Glu Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu
 450 455 460
 Ile Thr Asp Gly Pro Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys
 465 470 475 480
 Asn Ala Gly Glu Thr Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr
 485 490 495
 Val Lys Ile Gly Ser Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly
 500 505 510
 Ser Val Ser Ile Tyr Val Gln Lys
 515 520

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 548 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Val Leu Thr Phe His Arg Ile Ile Arg Lys Gly Trp Met Phe Leu Leu
 1 5 10 15
 Ala Phe Leu Leu Thr Ala Ser Leu Phe Cys Pro Thr Gly Arg His Ala
 20 25 30
 Lys Ala Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp
 35 40 45
 Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala
 50 55 60
 Asn Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Ser Leu Pro Pro Ala
 65 70 75 80
 Tyr Lys Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu
 85 90 95
 Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr
 100 105 110

Gly Thr Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala
 115 120 125
 Gly Met Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala
 130 135 140
 Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg
 145 150 155 160
 Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe
 165 170 175
 Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp
 180 185 190
 Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg
 195 200 205
 Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp
 210 215 220
 Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met
 225 230 235 240
 Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr
 245 250 255
 Val Asn Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Gly Leu Lys His
 260 265 270
 Ile Lys Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln
 275 280 285
 Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile
 290 295 300
 Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asn Gly Thr Met Ser Leu
 305 310 315 320
 Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly
 325 330 335
 Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp
 340 345 350
 Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Asn Pro
 355 360 365
 Ala Lys Arg Cys Ser His Gly Arg Pro Trp Phe Lys Pro Leu Ala Tyr
 370 375 380
 Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly
 385 390 395 400
 Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys
 405 410 415
 Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln
 420 425 430
 His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly
 435 440 445
 Val Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly
 450 455 460
 Ala Gly Arg Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys
 465 470 475 480
 Val Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn
 485 490 495
 Ser Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val
 500 505 510

Trp Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr
 515 520 525
 Thr Arg Pro Trp Thr Gly Glu Phe Val Arg Trp His Glu Pr Arg Leu
 530 535 540
 Val Ala Trp Pro
 545

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15
 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu
 20 25 30
 Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45
 Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60
 Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80
 Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
 85 90 95
 Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
 100 105 110
 Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
 115 120 125
 Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
 130 135 140
 Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160
 Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175
 Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Thr Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205
 Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220
 Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240
 Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
 245 250 255
 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
 260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285
 His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
 290 295 300
 Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335
 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350
 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365
 Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380
 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 385 390 395 400
 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415
 Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430
 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480
 Val Gln Arg

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala Ala Ala Ala Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu
 1 5 10 15
 Trp Tyr Met Pro Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp
 20 25 30
 Ser Ala Tyr Leu Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro
 35 40 45
 Ala Tyr Lys Gly Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp
 50 55 60
 Leu Tyr Asp Leu Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys
 65 70 75 80
 Tyr Gly Thr Lys Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser
 85 90 95

Arg Asp Ile Asn Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly
 100 105 110
 Ala Asp Ala Thr Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp
 115 120 125
 Arg Asn Arg Val Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His
 130 135 140
 Phe His Phe Pro Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His
 145 150 155 160
 Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn
 165 170 175
 Arg Ile Tyr Lys Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn
 180 185 190
 Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp
 195 200 205
 His Pro Asp Val Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala
 210 215 220
 Asn Glu Leu Gln Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile
 225 230 235 240
 Lys Phe Ser Phe Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr
 245 250 255
 Gly Lys Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly
 260 265 270
 Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe
 275 280 285
 Asp Val Pro Leu His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly
 290 295 300
 Gly Tyr Asp Met Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His
 305 310 315 320
 Pro Leu Lys Ser Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly
 325 330 335
 Gln Ser Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr
 340 345 350
 Ala Phe Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly
 355 360 365
 Asp Met Tyr Gly Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu
 370 375 380
 Lys His Lys Ile Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr
 385 390 395 400
 Gly Ala Gln His Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr
 405 410 415
 Arg Glu Gly Asp Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile
 420 425 430
 Thr Asp Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn
 435 440 445
 Ala Gly Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val
 450 455 460
 Val Ile Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser
 465 470 475 480
 Val Ser Ile Tyr Val Gln Arg
 485

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Lys Gln Gln Lys Arg Leu Thr Ala Arg Leu Leu Thr Leu Leu Phe
 1 5 10 15
 Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Ala Asn Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Arg Ser Lys Thr Leu Trp Ile Ser Leu Leu Phe Ala Leu Thr Leu
 1 5 10 15
 Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Ala Gly Lys
 20 25 30
 Ser

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Arg Ser Lys Thr Leu Trp Ile Ser Leu Leu Phe Ala Leu Thr Leu
 1 5 10 15
 Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Ala Ala Ala
 20 25 30
 Ala Ala Asn
 35

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Arg Ser Lys Thr Leu Trp Ile Ser Leu Leu Phe Ala Leu Thr Leu
 1 5 10 15
 Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Ala Asn Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACCTAATTA AAGCTTTCAC ACATTTTCAT TTT

33

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CACCTAATTA AAGCTTACAC ACATTTTCAT TTT

33

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCGCGTAATT TCCGGAGAAC ACCTAATTAA AGCCGCAACA CATTTCATT TTCCCGGGCG

60

CGGCAG

66

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
CCGGAGAACA CCTAATTAAA GCCCTAACAC ATTTTCATTT TC 42
- (2) INFORMATION FOR SEQ ID NO:46:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
CCGGAGAACA CCTAATTAAA GCCCACACAC ATTTTCATTT TC 42
- (2) INFORMATION FOR SEQ ID NO:47:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
CCGGAGAACA CCTAATTAAA GCCTGCACAC ATTTTCATTT TC 42
- (2) INFORMATION FOR SEQ ID NO:48:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
GATGCAGTAT TTCGAACTGG TATA 24
- (2) INFORMATION FOR SEQ ID NO:49:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
TGCCCAATGA TGGCCAACAT TGGAAG 26
- (2) INFORMATION FOR SEQ ID NO:50:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGAATGGTAT GCTCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGAATGGTAT CGCCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CGAATGGTAT AATCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGAATGGTAT GATCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGAATGGTAT CACCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGAATGGTAT AAACCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGAATGGTAT CCGCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGAATGGTAT TCTCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGAATGGTAC ACTCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CGAATGGTAT GTTCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGAATGGTAT TGTCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGAATGGTAT CAACCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGAATGGTAT GAACCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CGAATGGTAT GGTCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (gen mic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CGAATGGTAT ATTCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CGAATGGTAT TTTCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CGAATGGTAC TGGCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CGAATGGTAT TATCCCAATG ACGG

24

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CCGTCATTGG GACTACGTAC CATT

24

WHAT IS CLAIMED IS:

1. An improved bleach-containing cleaning composition, the improvement comprising adding to the bleach-containing composition a mutant alpha-amylase that is the expression product of a mutated DNA sequence encoding an alpha-amylase, the mutated DNA sequence being derived from a precursor alpha-amylase by the substitution of a methionine at a position equivalent to M+197 in *B. licheniformis* alpha-amylase and the substitution of one or more methionine or tryptophan at a position equivalent to M+15 or W+138 in *B. licheniformis* alpha-amylase.
2. An improved cleaning composition of Claim 1 wherein the cleaning composition is a dish care cleaning composition.
3. An improved cleaning composition of Claim 1 wherein the mutant alpha-amylase is selected from the group consisting of M15T/M197T; M15S/M197T; W138Y/M197T; M15S/W138Y/M197T and M15T/W138Y/M197T.
4. An improved cleaning composition of Claim 1 further comprising a mutant protease that is the expression product of a mutated DNA sequence encoding a protease, the mutated DNA sequence being derived from a precursor protease by the substitution of a methionine at a position equivalent to M+222 in *Bacillus amyloliquefaciens* protease.
5. An improved cleaning composition of Claim 4 wherein the mutant protease comprises a substitution selected from the group of amino acids consisting of alanine, cysteine and serine.
6. An improved cleaning composition of Claim 4 comprising an alpha-amylase mutant selected from the group consisting of M15T/M197T, M15S/M197T, W138Y/M197T, M15S/W138Y/M197T and M15T/W138Y/M197T, and a protease mutant selected from the group consisting of M222C, M222S and M222A.
7. An improved cleaning composition of Claim 6 which is a granular composition.

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10 30 50
AGCTTGAAGAAGTGAAGAAGCAGAGAGGCTATTGAATAAATGAGTAGAAAGCGCCATATC

70 90 110
GGCGCTTTTCTTTTGAAGAAAATATAGGGAAAATGGTACTTGTTAAAAATTCGGAATAT

130 150 170
TTATACAACATCATATGTTTCACATTGAAAGGGGAGGAGAATCATGAAACAACAAAAACG
M K Q Q K R

190 210 230
GCTTTACGCCCGATTGCTGACGCTGTTATTTGCGCTCATCTTCTTGCTGCCTCATTCTGC
L Y A R L L T L L F A L I F L L P H S A

250 270 290
AGCAGCGGCGGCAAATCTTAATGGGACGCTGATGCAGTATTTTGAATGGTACATGCCCAA
A A A A N L N G T L M Q Y F E W Y M P N

310 330 350
TGACGGCCAACATTGGAAGCGTTTGCAAACGACTCGGCATATTTGGCTGAACACGGTAT
D G Q H W K R L Q N D S A Y L A E H G I

370 390 410
TACTGCCGTCTGGATTCCCCCGGCATATAAGGGGAACGAGCCAAGCGGATGTGGGCTACGG
T A V W I P P A Y K G T S Q A D V G Y G

430 450 470
TGCTTACGACCTTTATGATTTAGGGGAGTTTCATCAAAAAGGGACGGTTCGGACAAAGTA
A Y D L Y D L G E F H Q K G T V R T K Y

490 510 530
CGGCACAAAAGGAGAGCTGCAATCTGCGATCAAAAGTCTTCATTCCCGCGACATTAACGT
G T K G E L Q S A I K S L H S R D I N V

550 570 590
TTACGGGGATGTGGTCATCAACCACAAAGGCGGCGCTGATGCGACCGAAGATGTAACCGC
Y G D V V I N H K G G A D A T E D V T A

610 630 650
GGTTGAAGTCGATCCCGCTGACCGCAACCGCGTAATTTTCAGGAGAACACCTAATTAAAGC
V E V D P A D R N R V I S G E H L I K A

670 690 710
CTGGACACATTTTCATTTTCCGGGGCGCGGCAGCACATACAGCGATTTTAAATGGCATTG
W T H F H F P G R G S T Y S D F K W H W

730 750 770
GTACCATTTTGACGGAACCGATTGGGACGAGTCCCGAAAGCTGAACCGCATCTATAAGTT
Y H F D G T D W D E S R K L N R I Y K F

790 810 830
TCAAGGAAAGGCTTGGGATTGGGAAGTTTCCAATGAAAACGGCAACTATGATTATTTGAT
Q G K A W D W E V S N E N G N Y D Y L M

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850 870 890
GTATGCCGACATCGATTATGACCATCCTGATGTCGCAGCAGAAATTAAGAGATGGGGCAC
Y A D I D Y D H P D V A A E I K R W G T

910 930 950
TTGGTATGCCAATGAACTGCAATTGGACGGTTTCCGTCTTGATGCTGTCAAACACATTAA
W Y A N E L Q L D G F R L D A V K H I K

970 990 1010
ATTTTCTTTTTTGC GGGATTGGGTTAATCATGT CAGGGAAAAACGGGGGAAGGAAATGTT
F S F L R D W V N H V R E K T G K E M F

1030 1050 1070
TACGGTAGCTGAATATTGGCAGAATGACTTGGGCGCGCTGGAAAAC TATTTGAACAAAAC
T V A E Y W Q N D L G A L E N Y L N K T

1090 1110 1130
AAATTTTAATCATT CAGTGTTTGACGTGCCGCTTCATTATCAGTTCCATGCTGCATCGAC
N F N H S V F D V P L H Y Q F H A A S T

1150 1170 1190
ACAGGGAGGCGGCTATGATATGAGGAAATTGCTGAACGGGTACGGTCGTTTCCAAGCATCC
Q G G G Y D M R K L L N G T V V S K H P

1210 1230 1250
GTTGAAATCGGTTACATTTGTCGATAACCATGATACACAGCCGGGGCAATCGCTTGAGTC
L K S V T F V D N H D T Q P G Q S L E S

1270 1290 1310
GACTGTCCAAACATGGTTTAAGCCGCTTGCTTACGCTTTTATTCTCACAAGGGAATCTGG
T V Q T W F K P L A Y A F I L T R E S G

1330 1350 1370
ATACCCTCAGGTTTTCTACGGGGATATGTACGGGACGAAAGGAGACTCCCAGCGCGAAAT
Y P Q V F Y G D M Y G T K G D S Q R E I

1390 1410 1430
TCCTGCCTTGAAACACAAAATTGAACCGATCTTAAAGCGAGAAAACAGTATGCGTACGG
P A L K H K I E P I L K A R K Q Y A Y G

1450 1470 1490
AGCACAGCATGATTATTTGACCAACCATGACATTGTCTGGCTGGACAAGGGAAGGCGACAG
A Q H D Y F D H H D I V G W T R E G D S

1510 1530 1550
CTCGGTTGCAAATTCAGGTTTGGCGGCATTAATAACAGACGGACCCGGTGGGGCAAAGCG
S V A N S G L A A L I T D G P G G A K R

1570 1590 1610
AATGTATGTCGGCCGGCAAACGCCGGTGAGACATGGCATGACATTACCGGAAACCGTTC
M Y V G R Q N A G E T W H D I T G N R S

1630 1650 1670
GGAGCCGTTGTCATCAATTCGGAAGGCTGGGGAGAGTTTCACGTAAACGGCGGGTCGGT
E P V V I N S E G W G E F H V N G G S V

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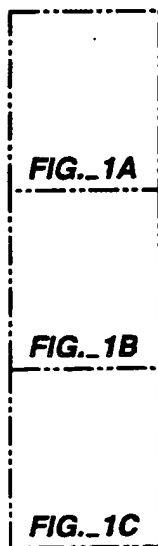
1690 1710 1730
TTCAATTTATGTTCAAAGATAGAAGAGCAGAGAGGACGGATTTCCTGAAGGAAATCCGTT
S I Y V Q R *

1750 1770 1790
TTTTTATTTTGCCCGTCTTATAAATTTCTTTGATTACATTTTATAATTAATTTTAACAAA

1810 1830 1850
GTGTCATCAGCCCTCAGGAAGGACTTGCTGACAGTTTGAATCGCATAGGTAAGGCGGGGA

1870 1890 1910
TGAAATGGCAACGTTATCTGATGTAGCAAAGAAAGCAAATGTGTGCGAAAATGACGGTATC

1930 1950
GCGGGTGATCAATCATCCTGAGACTGTGACGGATGAATTGAAAAAGCT

FIG._1C**FIG._1**

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10 30 50
ANLNGTLMQYFEWYMPNDGQHWKRLQND SAYLA EHGITAVWIPPAYKGT SQADVG YGAYD

70 90 110
LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKG GADATEDVTAVEV

130 150 170
DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQ GK

190 210 230
AWDWEVSNENGN YDYL MYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF

250 270 290
LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNH SVFDVPLHYQFHAASTQGG

310 330 350
GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTFWKPLAYAFILTRESGY PQ

370 390 410
VFGDMYGTGKGSQREIPALKHKIEPILKARKQYAYGAQH DYFDHHDIVGWTREGDSSVA

430 450 470
NSGLAALITDGP GGAKR MYVGRQNA GETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY

VQR

FIG._2

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Am-Lich = <i>B. Licheniformis</i>	Am-Amylo = <i>B. amyloliquefaciens</i>	Am-Stearo = <i>B. stearothermophilus</i>
1 Am-Lich Am-Amylo Am-StearoMKQQ KRLYARLLTL LFALIFLLPH MRGRGNMIQK RKRTVSFRLV LMCTLLFVSLVLTF HRIIRKGWMF LLAFLLTASLSAAA AANLNGTLMQ YFEWYMPNDGPITK TSAVNGTLMQ YFEWYTPNDG FCPTGRHAKA AAPFNGTMMQ YFEWYLPDDG
61 Am-Lich Am-Amylo Am-Stearo	QHWKRLQND AYLAEHGITA VWIPPAYKGT QHWKRLONDA EHLSDIGITA VWIPPAYKGL TLWTKVANE A NNLSSLGITA LSLPPAYKGT	79 120 QGVTVRTKYGT QGVTVRTKYGT QGVTVRTKYGT
121 Am-Lich Am-Amylo Am-Stearo	KGELQSAIKS LHSRDINVYG DVVINHKGGA DATEDVTAVE KSELQDAIGS LHSRNVQVYG DVVLNHKAGA DATEDVTAVE KAQYLQAIQA AHAAAGMQVYA <u>DWFDHKGGA</u> DGTEWDAVE	139 180 SGEHLIKAWT SEEYQIKAWT SGTYQIQAWT
181 Am-Lich Am-Amylo Am-St aro	HFHFPGRGST YSDFKWHWYH FDGTDWDESR KLNRIYKF.... DFRFPGRGNT YSDFKWHWYH FDGADWDESR KISRIFKFRG KFDFPGRGNT YSDFKWRWYH FDGVDWDESR KLSRIYKFRG	197 240 NENGNVDYLM SENGNYDYLM TENGNVDYLM
241 Am-Lich Am-Amylo Am-St aro	YADIDYDHPD VAAEIKRWGT WYANELQLDG FRLDAVKHIK YADVVDYDHPD VVAETKKWGI WYANELSLDG FRIDAAKHK YADLMDHPE VVTELKNWKG WYVNTTNIDG <u>FRLDGLKHK</u>	257 300 VREKTKEMF VRQATGKEMF VRSQTGKPLE
301 Am-Lich Am-Amylo Am-Stearo	TVAEYWQNDL GALENYLNKT NFNHVSFVDP LHYQFHAAST QGGGYDMRKL TVAEYWQNN A GKLENYLNKT SFNQSVFVDP LHFNLQAASS QGGGYDMRRL <u>TVGEYWSYDI</u> NKLHNYITKT NGTMSLFDAP LHNKFYTASK SGGAFDMRTL	317 360 LNGTVVSKHP LDGTVVSRHP MTNTLMKDQP

FIG. 3A

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Am-Lich	361	LKSVTFVDNH	DTQPGQSLES	TVQTWFKPLA	YAFILTRESG	YPQVFYGDY	GTKGDSQREI	377
Am-Amylo		EKAVTFVENH	DTQPGQSLES	TVQTWFKPLA	YAFILTRESG	YPQVFYGDY	GTKGTSPKEI	420
Am-Stearo		TLAVTFVDNH	DINPAKR..CS	HGRPWFKPLA	YAFILTRQEG	YPCVFYGDY	GI.....PQYNI	
Am-Lich	421	PALKHKIEPI	LKARKQYAYG	AQHDYFDHHD	IVGWTREGDS	SVANSGLAAL	ITDGPGGAKR	437
Am-Amylo		PSLKDNIPI	LKARKEYAYG	PQHDYIDHPD	VIGWTREGDS	SAAKSGLAAL	ITDGPGGSKR	480
Am-Stearo		PSLKSIDPL	LIARRDYAYG	TQHDYLDHSD	IIGWTREGVT	EKPGSGLAAL	ITDGAGRSKW	
Am-Lich	481	MYVGRQNAGE	TWHDITGNRS	EPVVINSEGW	GEFHVNGGSV	SIYVQR.....		540
Am-Amylo		MYAGLKNAGE	TWYDITGNRS	DTVKIGSDGW	GEFHVNDGSV	SIYVQK.....		
Am-Stearo		MYVGKQHAGK	VFYDLTGNRS	DTVINSDBGW	GEFKVNGGSV	SVWVPRKTTV	STIARPITTR	
Am-Lich	541							
Am-Amylo								
Am-St aro								

FIG.-3B

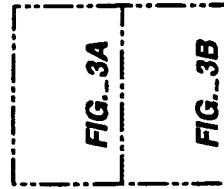


FIG.-3

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10 30 50
ANLNGTLMQYFEWYMPNDGQHWKRLQND SAYLAEHGITAVWIPPAYKGTSQADVGYGAYD

70 90 110
LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKG GADATEDVTAVEV

130 150 170
DPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWHYHFDGTDWDESRKLNRIYKFQ GK

190 210 230
AWDWEVSNENGN YDYLTYADIDYDHPDVA AEIKRWGTWYANELQLDGFRLDAVKHIKFSF

250 270 290
LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNH SVFDVPLHYQFHAASTQGG

310 330 350
GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQ TWFKPLAYAFILTRESGY PQ

370 390 410
VFYGD MYGT KGDSQREIPALKHKIEPILKARKQYAYGAQH DYFDHHDIVGWTREGDSSVA

430 450 470
NSGLAALITDGP GAKRMVYVGRQ NAGETWHDITGNRSEPVVINSEGWGEFHVNGG SVSIY

VQR

FIG._4a

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AAAA

14 34 54
ANLNGTLMQYFEWYMPNDGQHWKRLQND SAYLAEHGITAVWIPPAYKGTSQADVGYGAYD

74 94 114
LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKG GADATEDVTAVEV

134 154 174
DPADRNRVISGEHLIKAWTHFHPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQ GK

194 214 234
AWDWEVSNENGN YDYL MYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF

254 274 294
LRDWVNHVREKTGKEMFTVAEYWQNDLGALENYLNKTNFNH SVFDVPLHYQFHAASTQGG

314 334 354
GYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQ TWFKPLAYAFILTRESGYPO

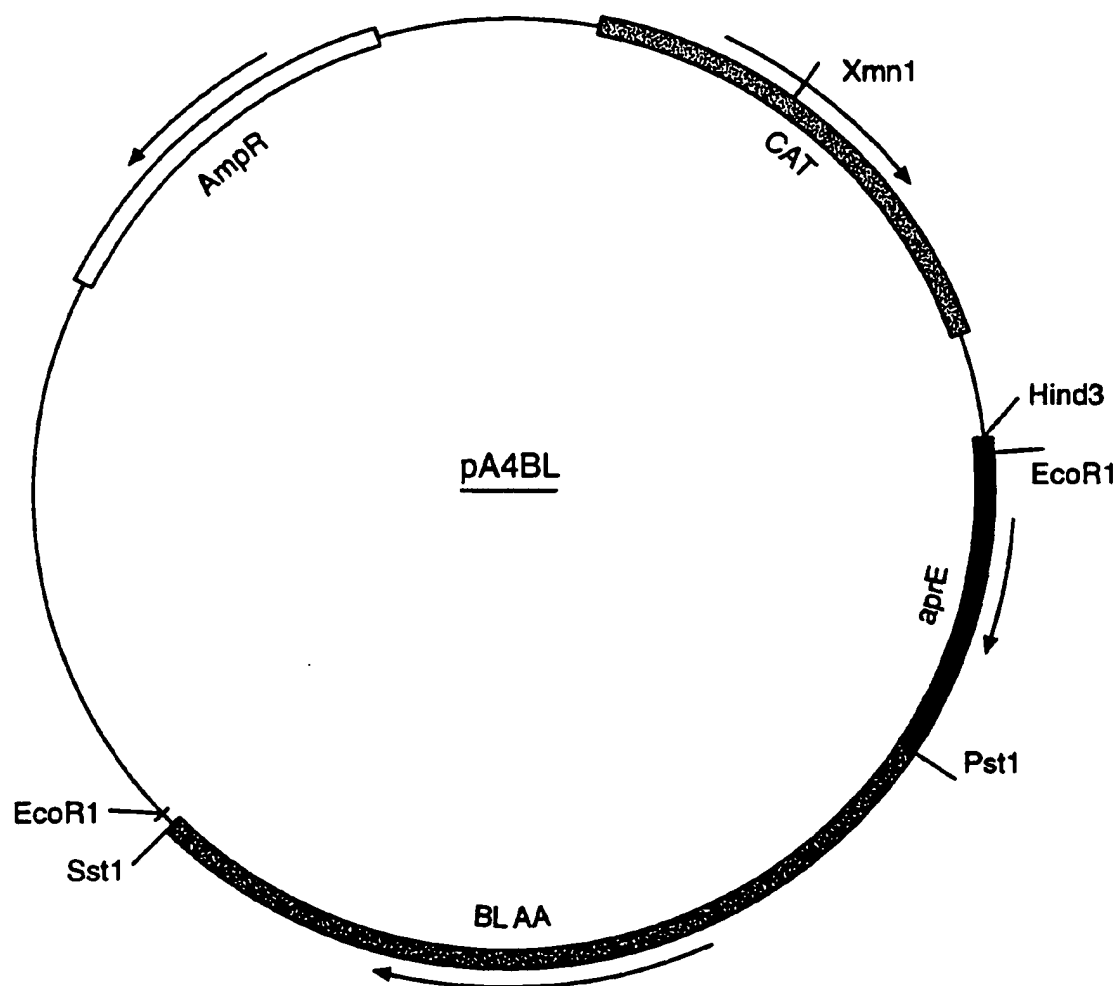
374 394 414
VFYGD MYGT KGDSQREIPALKHKIEPILKARKQYAYGAQH DYFDHHDIVGWTREGDSSVA

434 454 474
NSGLAALITDGP GGAKR MYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIY

VQR

FIG._4b

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**FIG. 5**

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SIGNAL SEQUENCE - MATURE PROTEIN JUNCTIONS IN:*B.licheniformis* alpha-amylase.

MKQQKRLTARLLTLLFALIFLLPHSAAAA[ANL.....
 (PstI) ↓
 N-terminus

B.subtilis alkaline protease aprE.

MRSKTLWISLLFALTLLFTMAFSNMSAQA[AGKS.....
 (PstI) ↓
 N-terminus

B.licheniformis alpha-amylase in pA4BL.

MRSKTLWISLLFALTLLFTMAFSNMSAQA[AAAAAN.
 (PstI) ↓
 N-terminus

B.licheniformis alpha-amylase in pBLapr.

MRSKTLWISLLFALTLLFTMAFSNMSAQA[ANL.....
 N-terminus

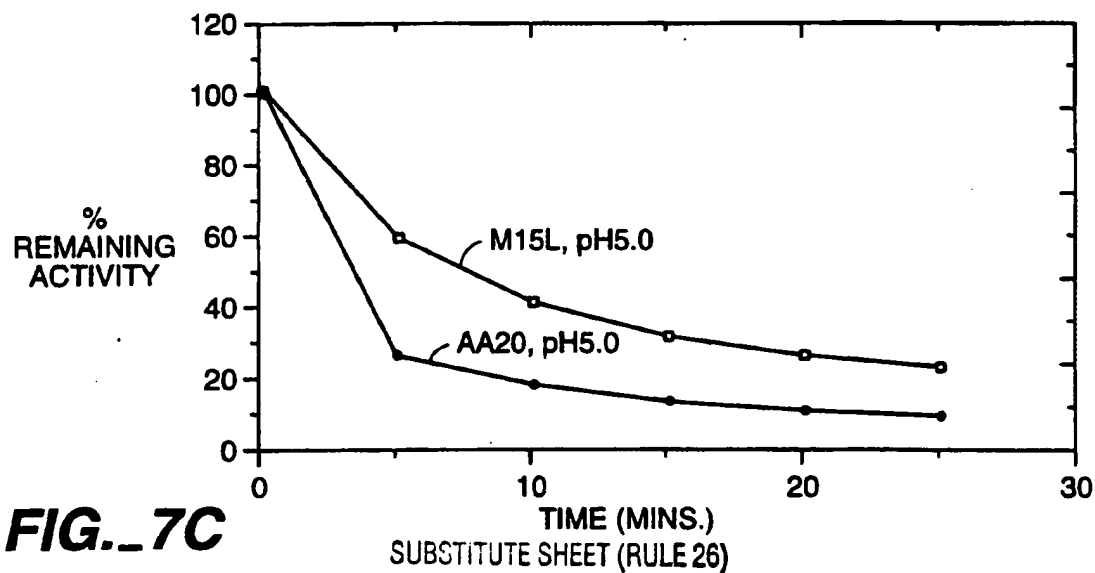
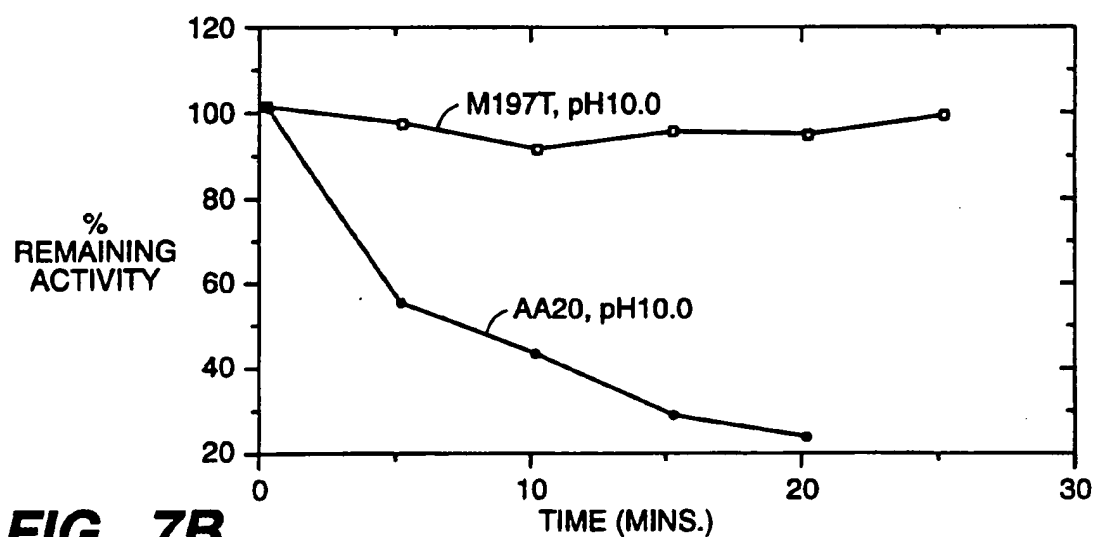
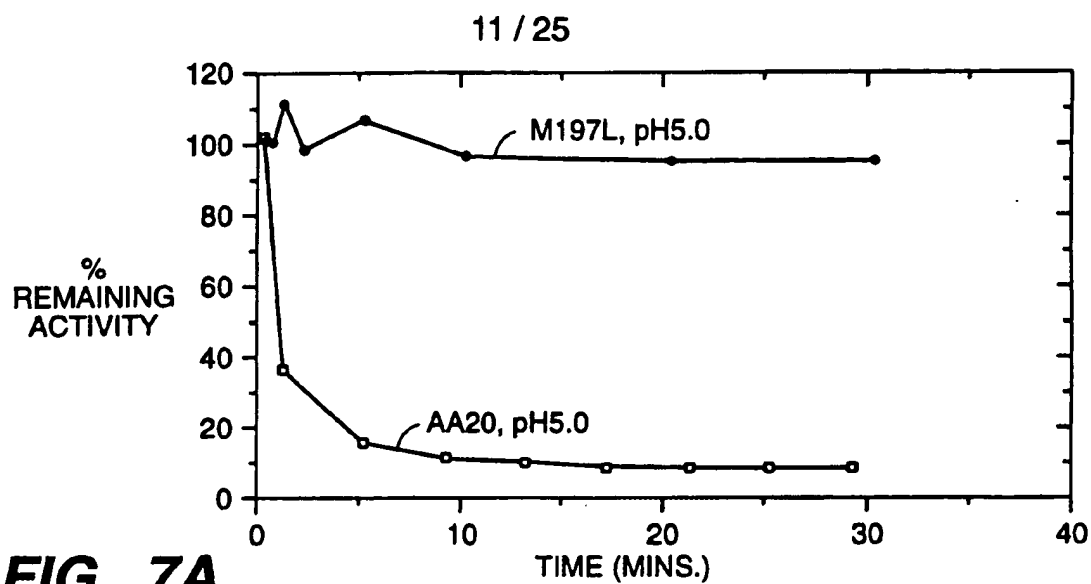
(PstI) indicates the site of the restriction site in the gene.

↓

[

N-terminus indicates cleavage site between signal peptide and secreted protein.

FIG._6



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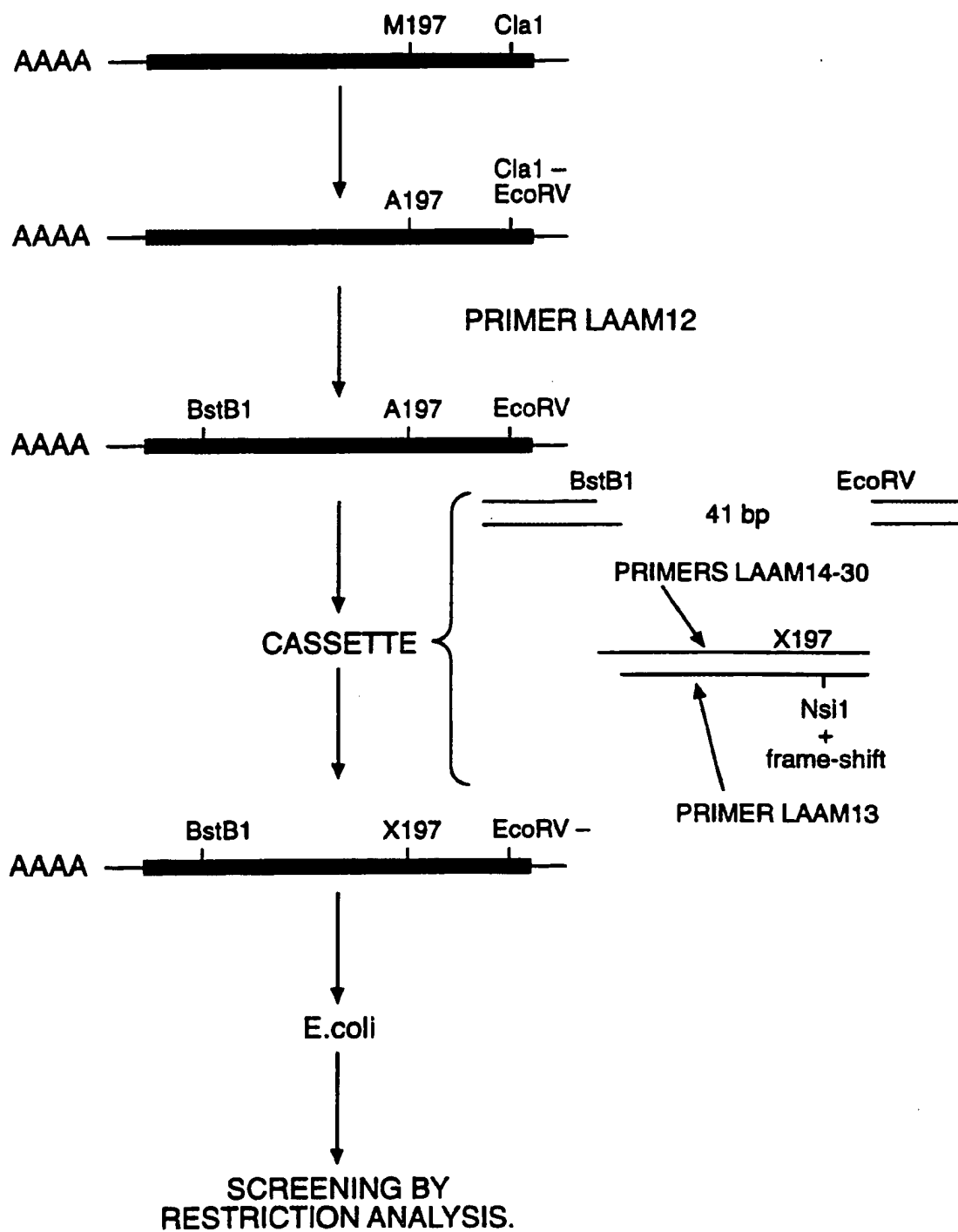
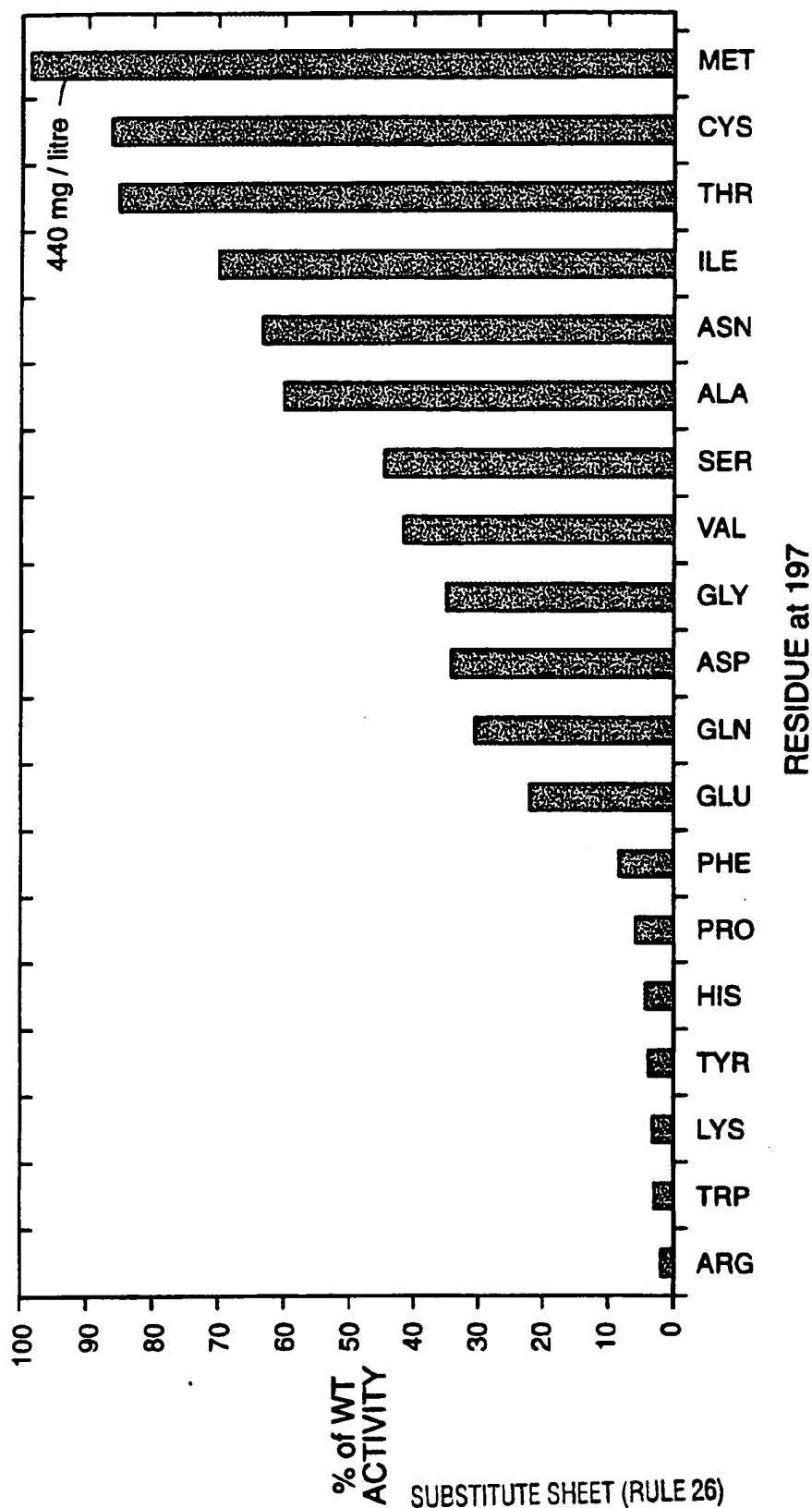


FIG. 8

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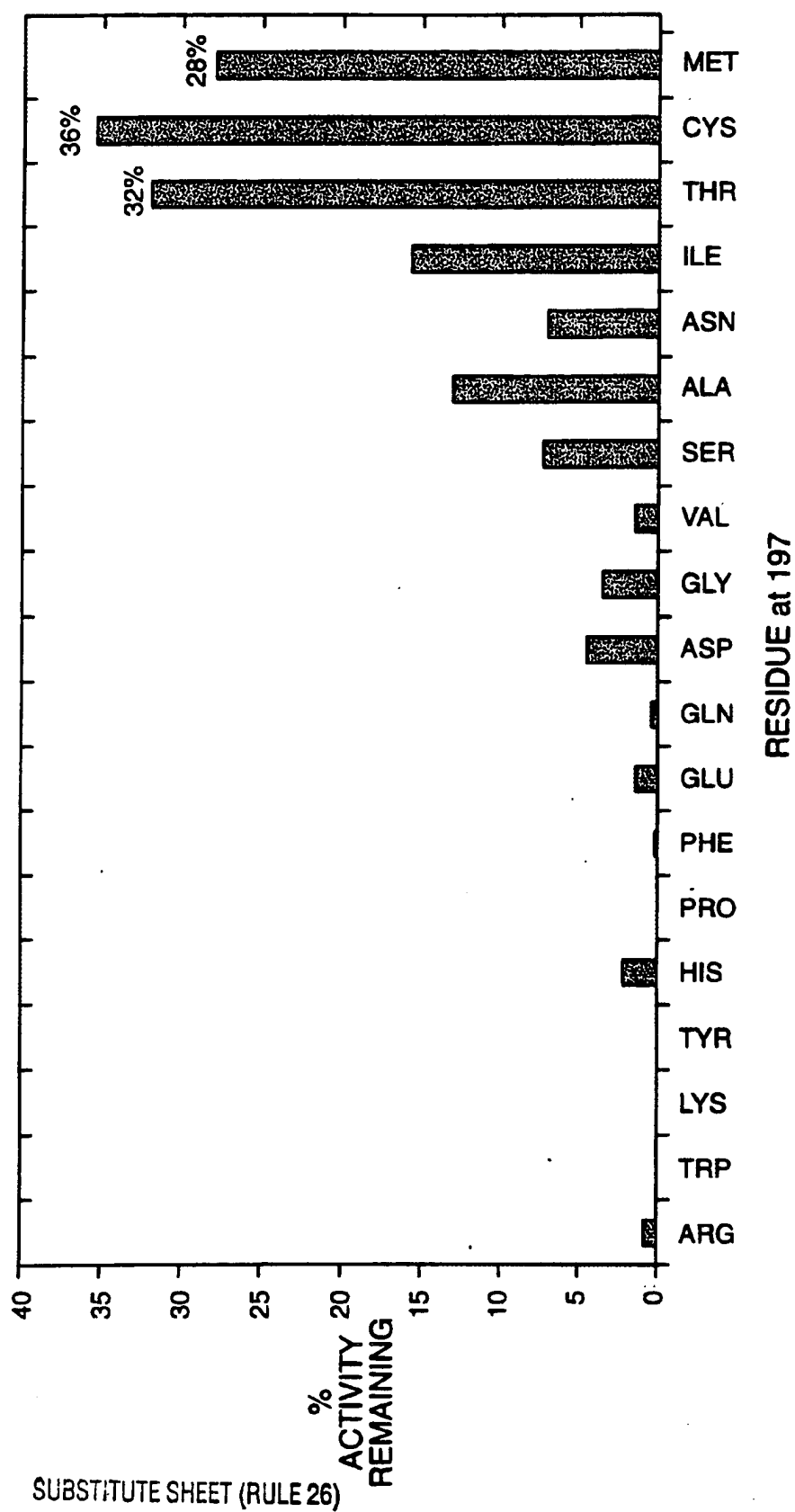
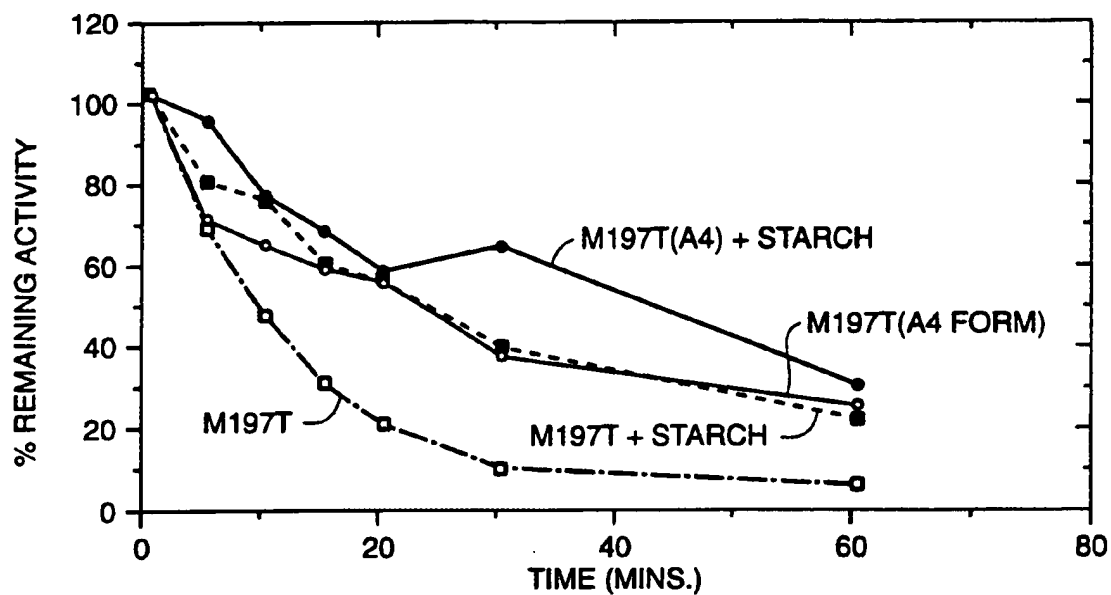
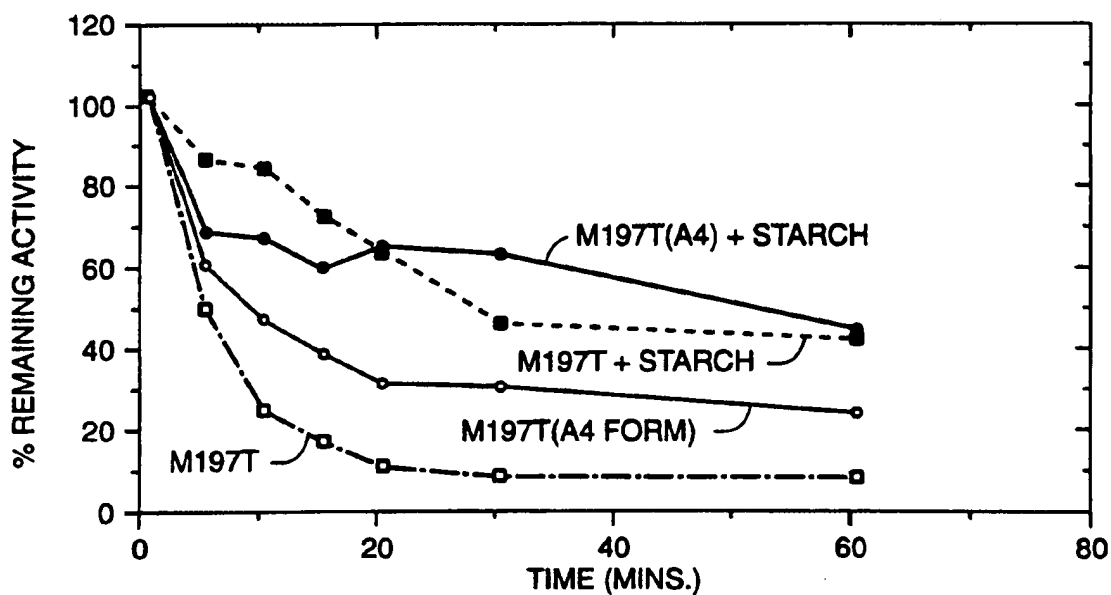
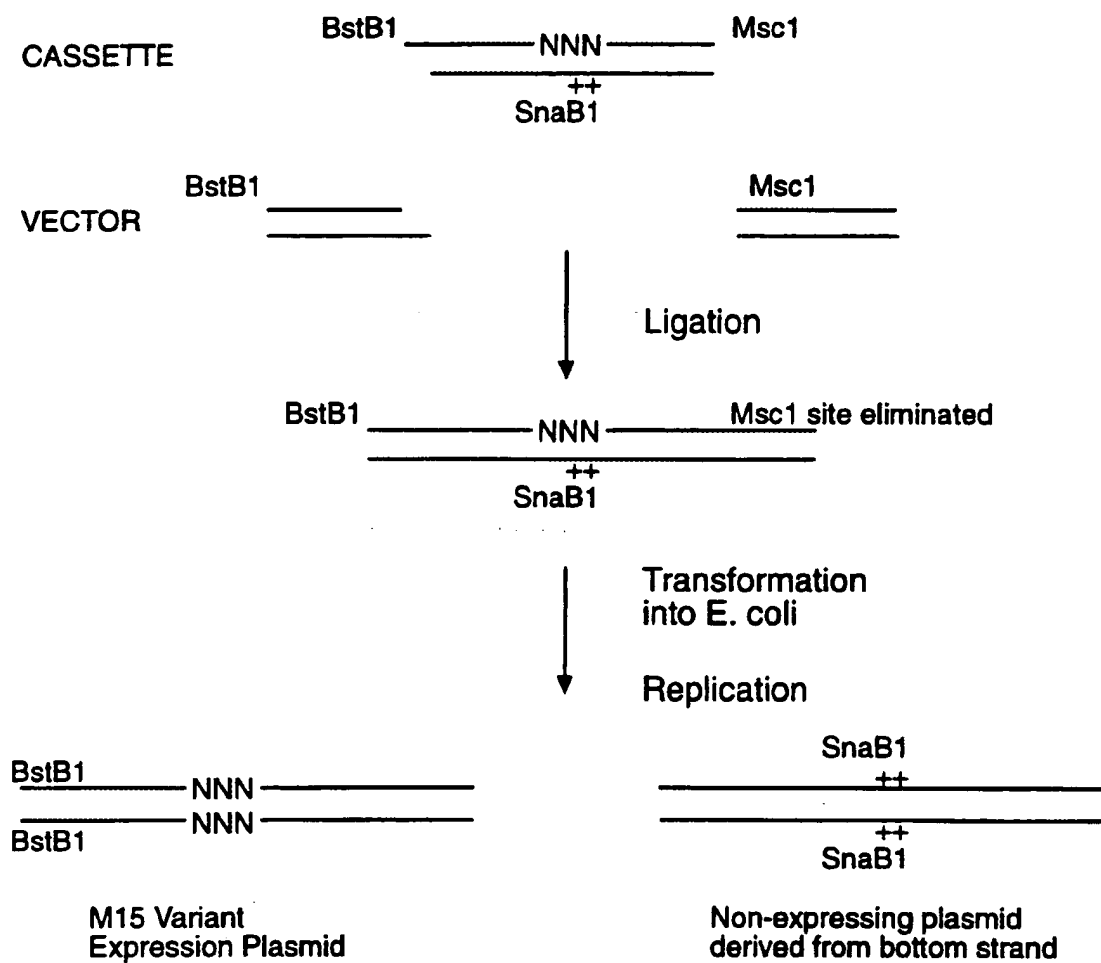


FIG.-10

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**FIG. 11A****FIG. 11B**

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**FIG. 12**

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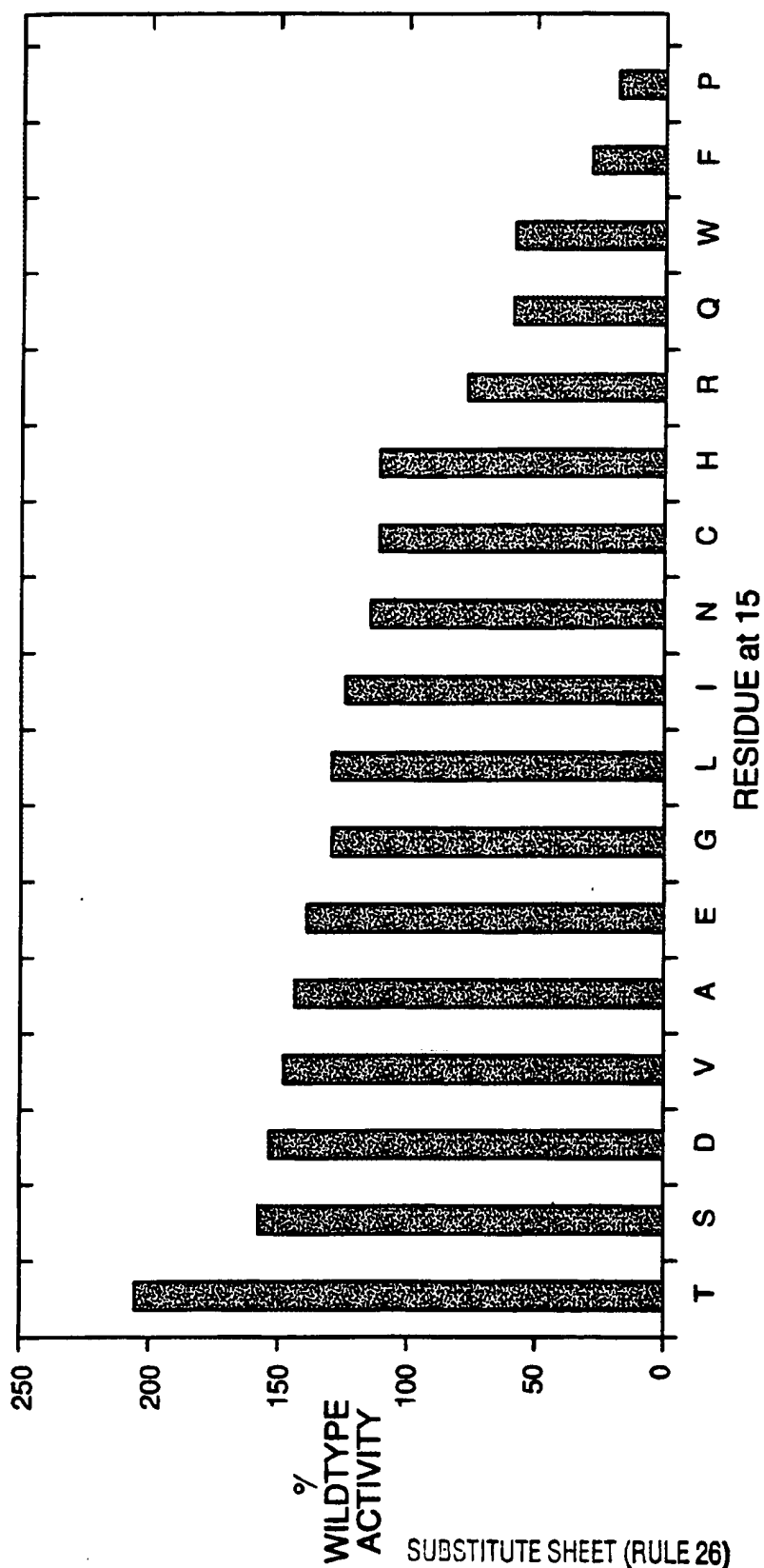


FIG. 13

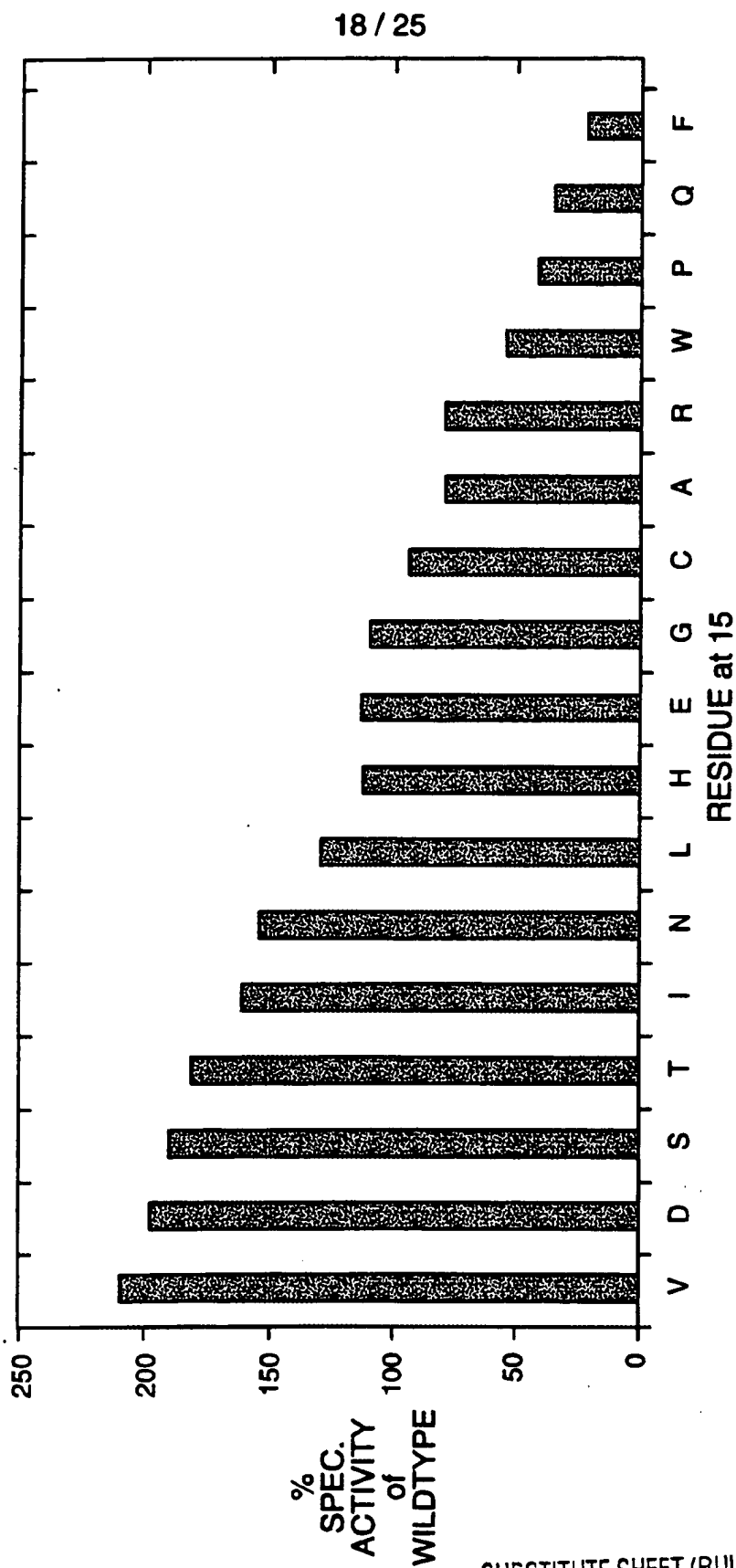


FIG. 14

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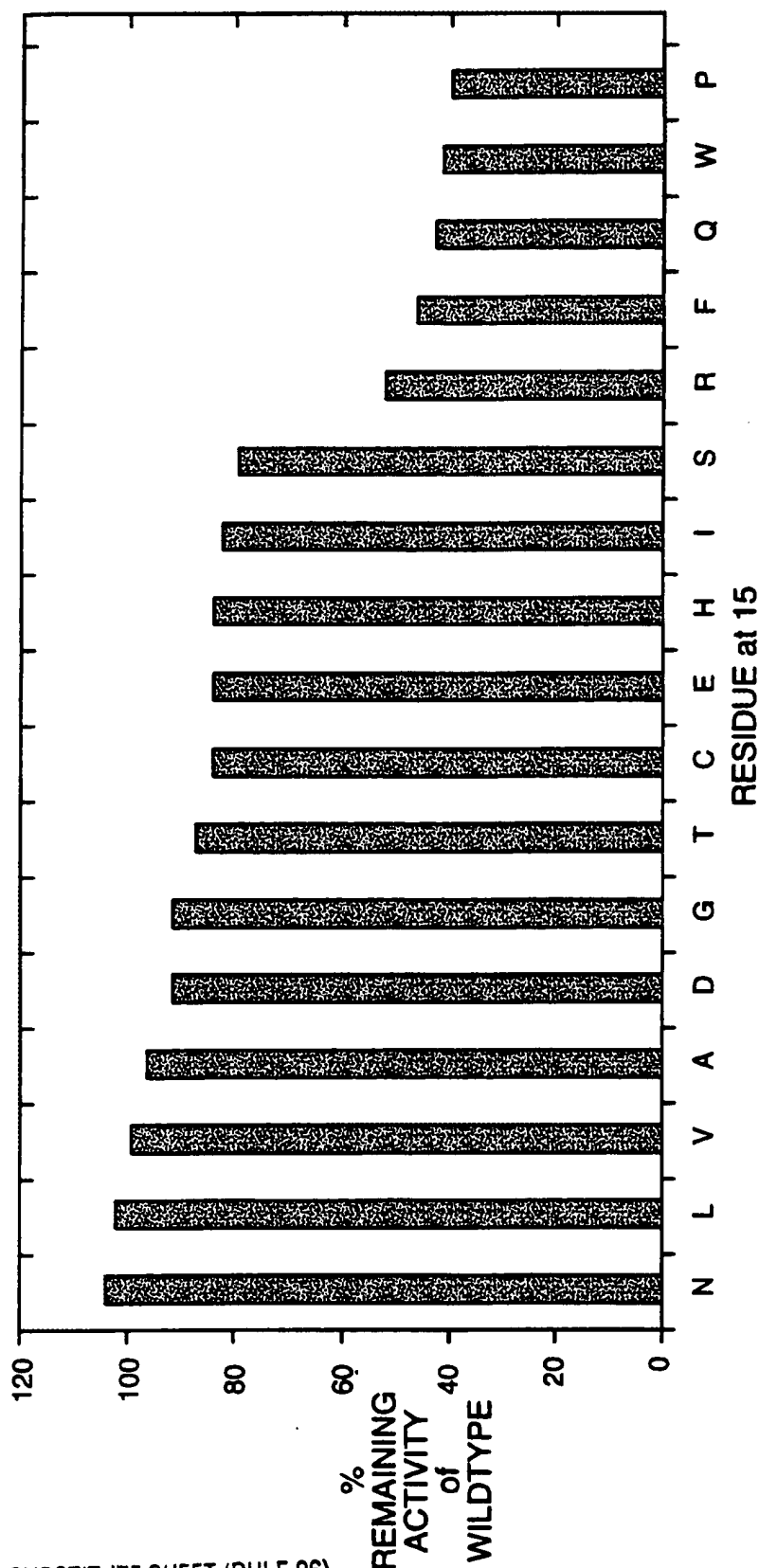


FIG.-15

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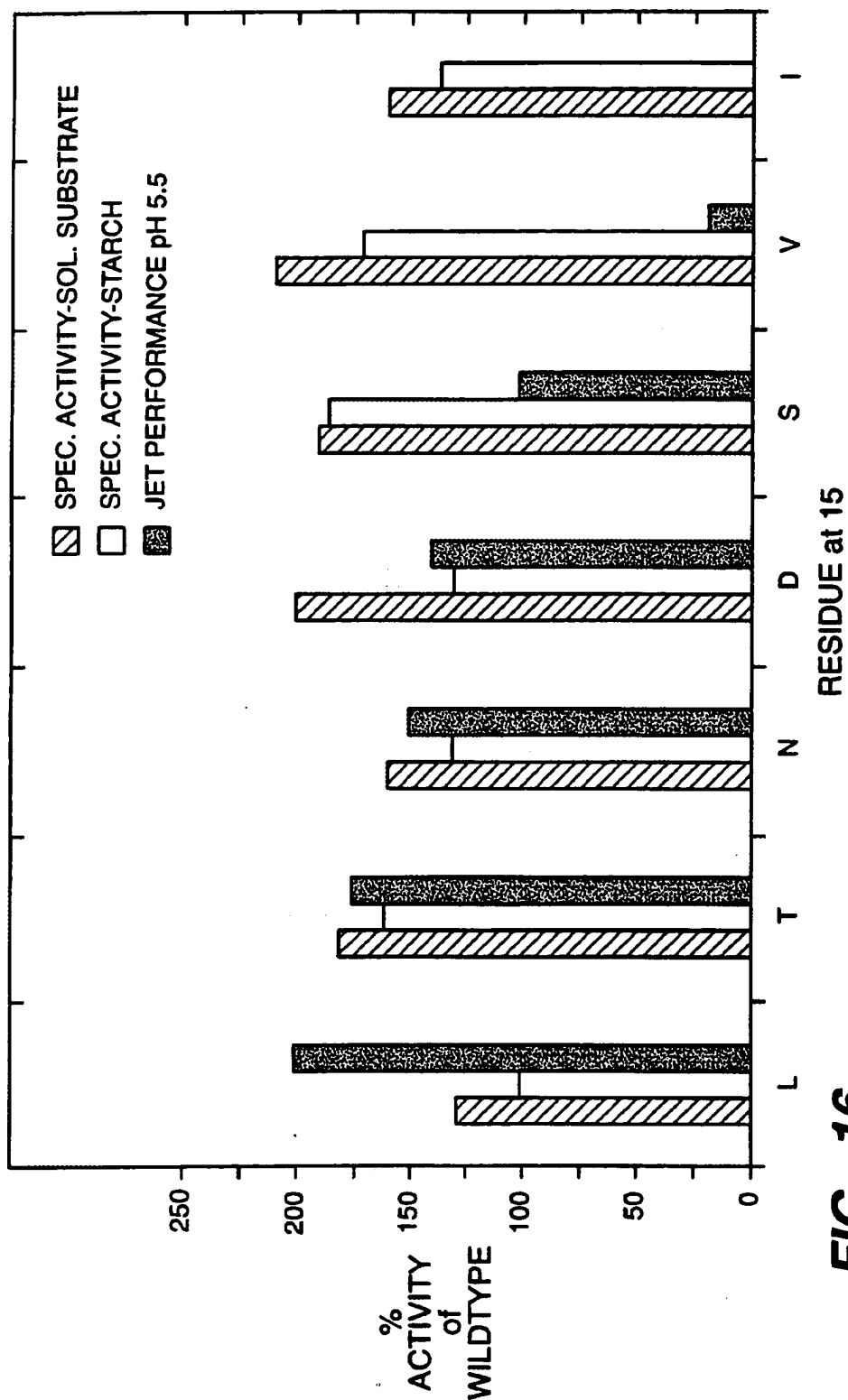
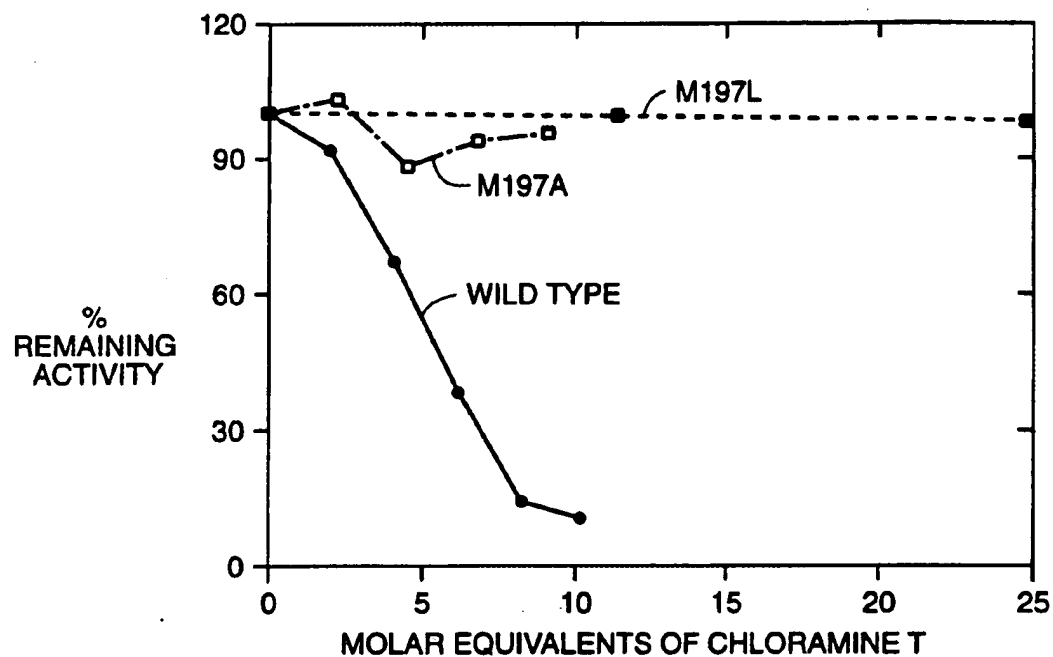
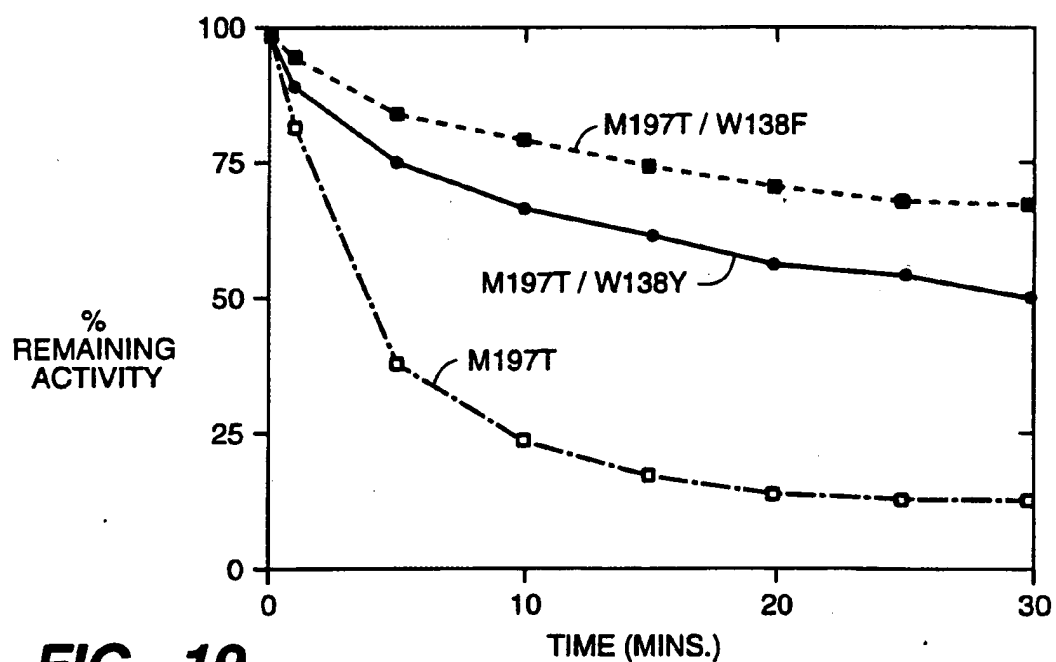
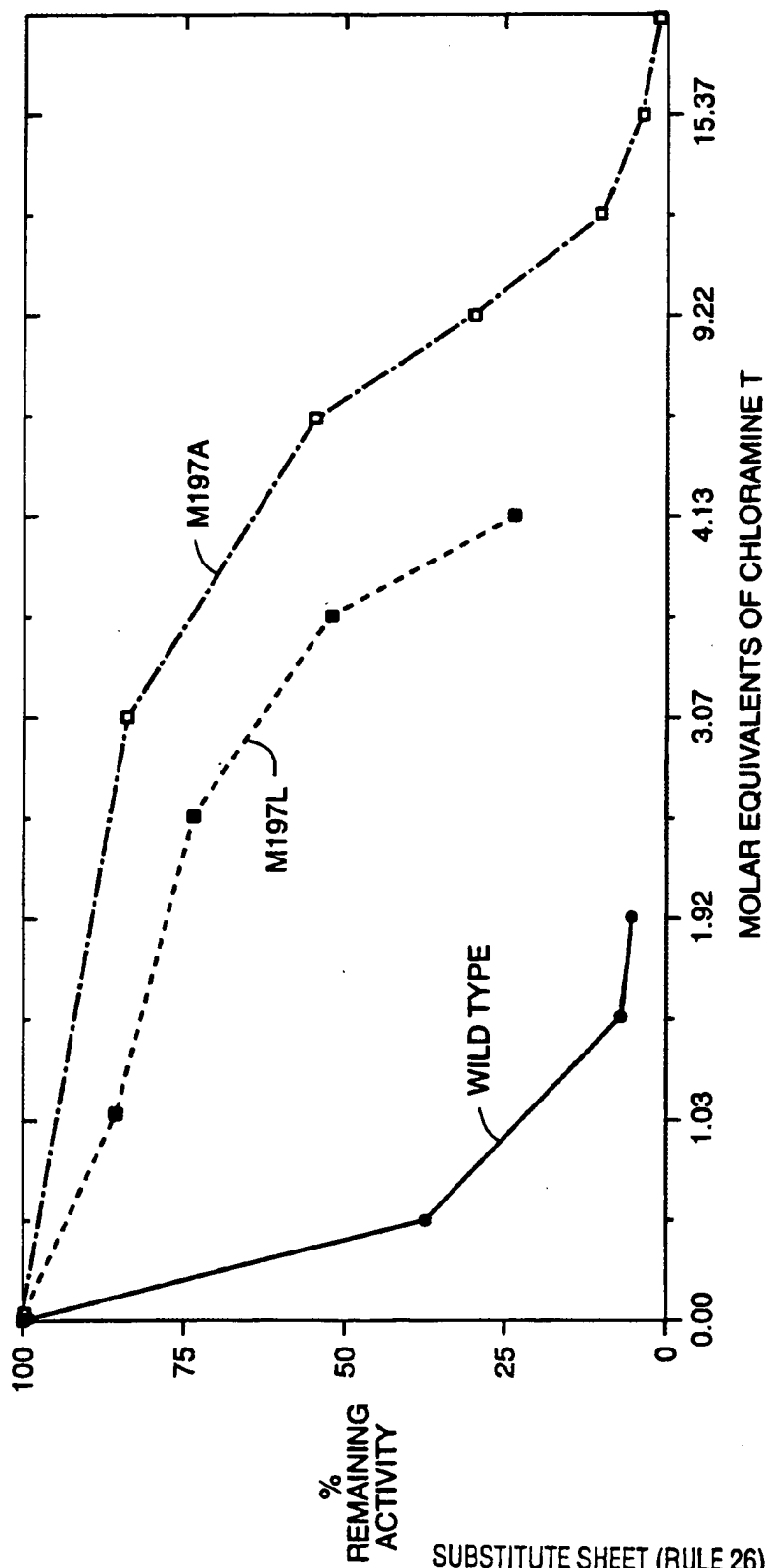


FIG.-16

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**FIG. 17****FIG. 19**

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**FIG. 18**

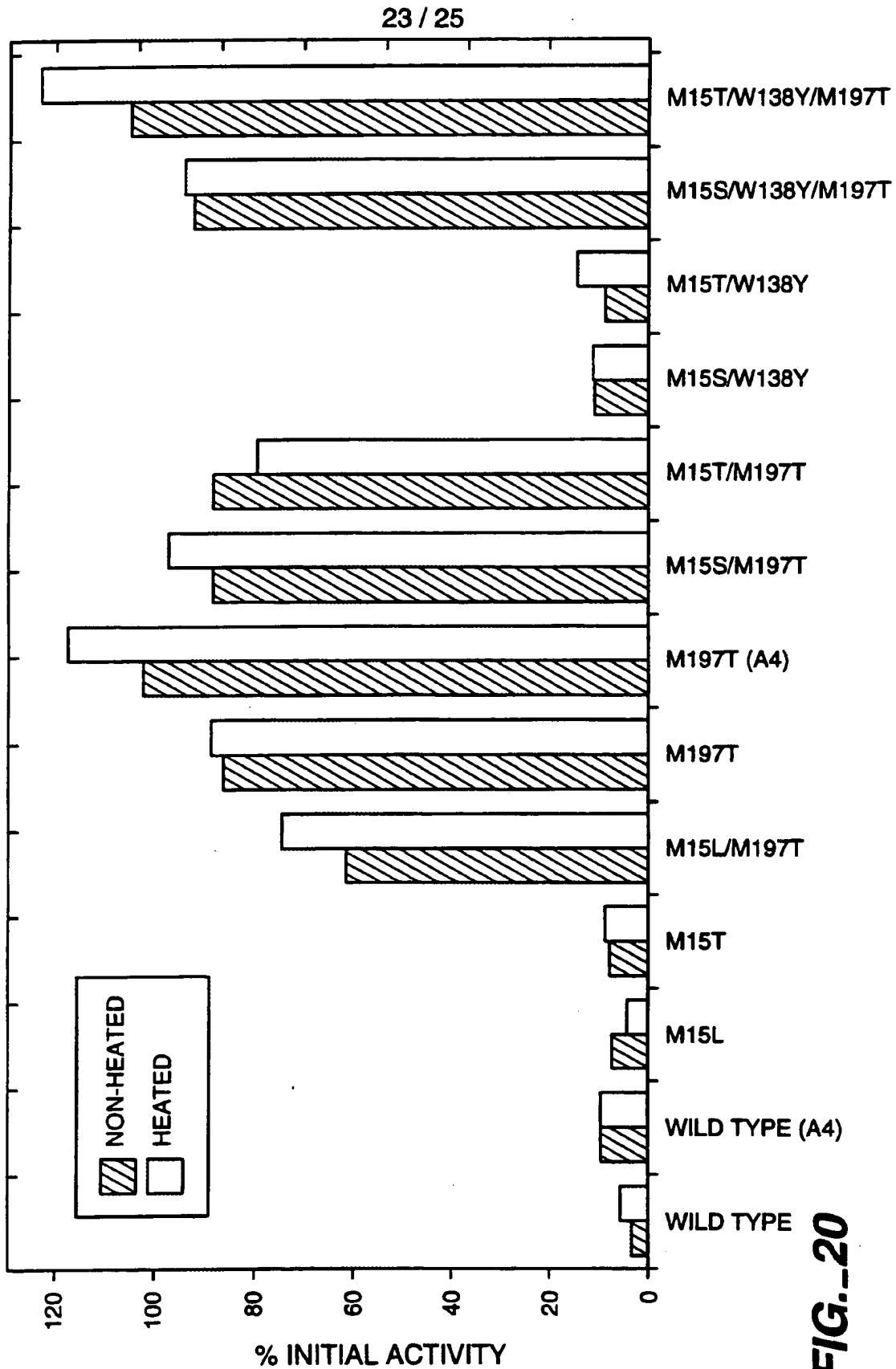


FIG.-20

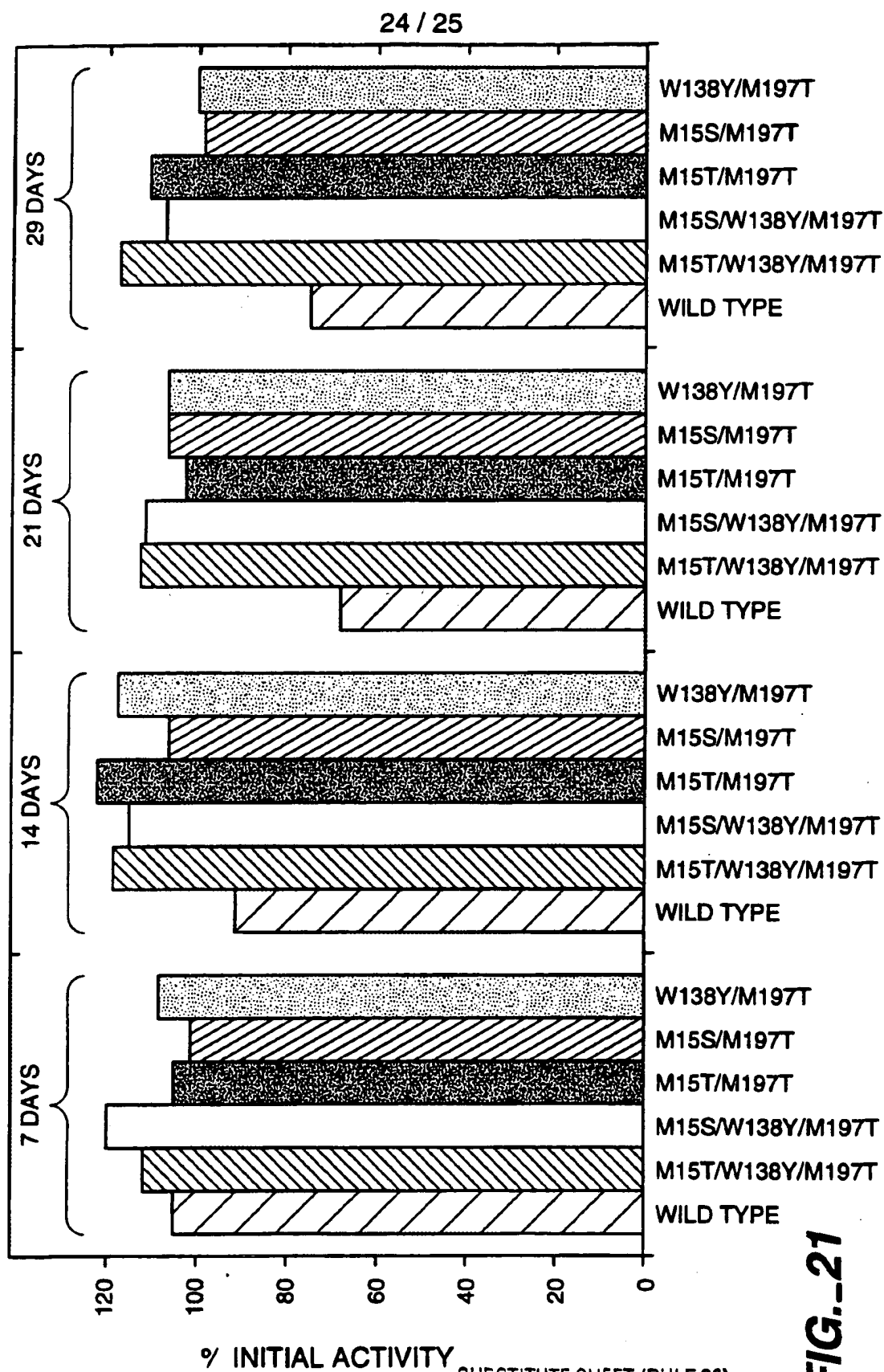
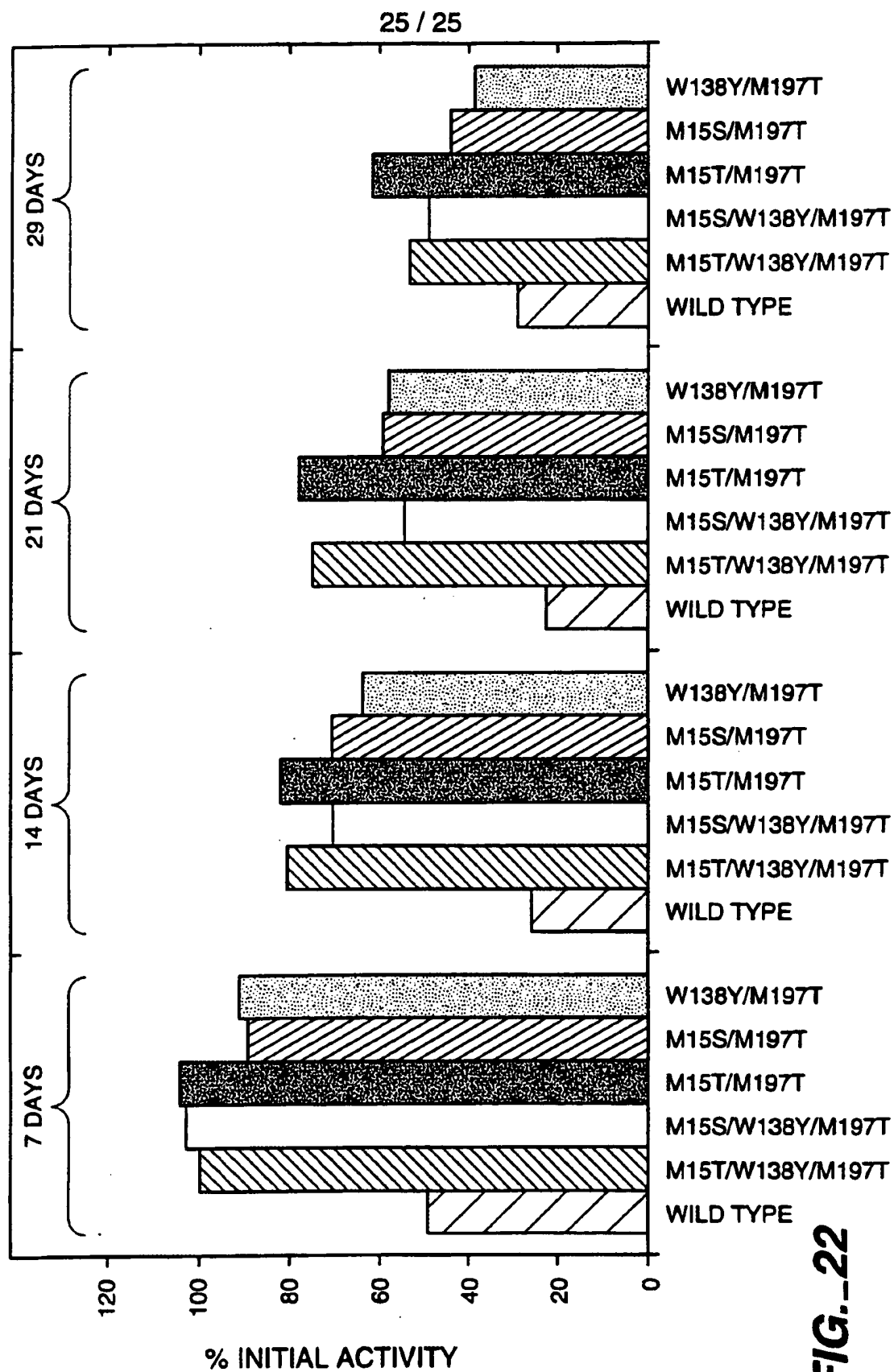


FIG.-21



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FIG.-22

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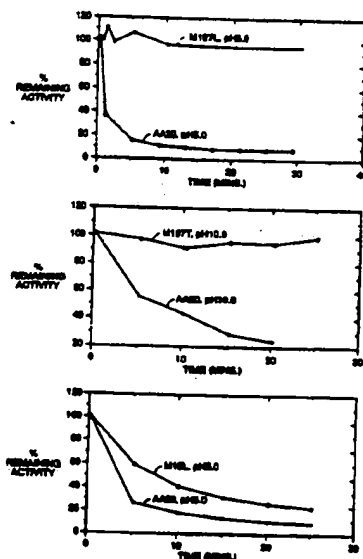
(81) Designated States: AU, BR, CA, CN, CZ, FI, HU, JP, KR, MX, NO, NZ, PL, RU, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

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(57) Abstract

Novel alpha-amylase mutants derived from the DNA sequences of naturally occurring or recombinant alpha-amylases are disclosed. The mutant alpha-amylases, in general, are obtained by *in vitro* modifications of a precursor DNA sequence encoding the naturally occurring or recombinant alpha-amylase to generate the substitution (replacement) or deletion of one or more oxidizable amino acid residues in the amino acid sequence of a precursor alpha-amylase. Such mutant alpha-amylases have altered oxidative stability and/or altered pH performance profiles and/or altered thermal stability as compared to the precursor. Also disclosed are detergent and starch liquefaction alpha-amylases from *Bacillus licheniformis* modified at MET197 or MET15 or at TRP138 residues or at equivalent residues of other alpha-amylases from other microbial sources (*Bacillus*, *Aspergillus*).

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 95/10426

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 6 C12N9/28 C12N9/54 C11D3/386

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A	---	3-7
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